WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Friday, August 19, 2005

Hide?	Set Name	Query	Hit Count
	DB=PGPB,USPT; PLUR=YES; OP=OR		
☐	L25	linker and L24	1
☐	L24	6403371.pn.	1
☐	L23	6403371	1
☐	L22	library with linkers with (several or many or plurality or multiple)	166
☐	L21	library with linkers with (several or two or many or plurality or multiple)	303
☐	L20	library with linkers	2837
☐	L19	library with linker	2837
☐	L18	library same ($nucleotide with linker with (random or degenerate))	124
☐	L17	$nucleotide with linker with (random or degenerate)	234
☐	L16	linker with (random or degenerate)	932
☐	L15	linker with random with degenerate	5
☐	L14	(varying or vary or variable) with (length or number) and 5260203.pn.	1
☐	L13	(varying or vary or variable) and 5260203.pn.	1
☐	L12	l10 not L11	1
☐	L11	linker and L10	5
☐	L10	5747334.pn. or L9	6
☐	L9	5443953.pn. or 5585089.pn. or 5260203.pn. or 4816567.pn. or 5624821.pn. or 5013653.pn	5
☐	L8	5747334.pn.	1
☐	L7	linker with $nucleotide with ((variable or vary or varying) with number)	10
☐	L6	linker with $nucleotide with ((variable or vary or varying) with length)	65
☐	L5	library same $nucleotide same ((variable or vary or varying) with length) same linker	21
☐	L4	library same (linker with $nucleotide with ((variable or vary or varying) with length))	1
☐	L3	library with $nucleotide with ((variable or vary or varying) with length)	33
☐	L2	library same $nucleotide same ((variable or vary or varying) with length)	229
☐	L1	library same $nucleotide same (variable with length)	39

END OF SEARCH HISTORY

WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Friday, August 19, 2005

Hide?	Set Name	Query	Hit Count
	DB=PGPB,USPT; PLUR=YES; OP=OR		
☐	L7	linker with $nucleotide with ((variable or vary or varying) with number)	10
☐	L6	linker with $nucleotide with ((variable or vary or varying) with length)	65
☐	L5	library same $nucleotide same ((variable or vary or varying) with length) same linker	21
☐	L4	library same (linker with $nucleotide with ((variable or vary or varying) with length))	1
☐	L3	library with $nucleotide with ((variable or vary or varying) with length)	33
☐	L2	library same $nucleotide same ((variable or vary or varying) with length)	229
☐	L1	library same $nucleotide same (variable with length)	39

END OF SEARCH HISTORY

WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Friday, August 19, 2005

Hide?	Set Name	Query	Hit Count
	DB=PGPB,USPT; PLUR=YES; OP=OR		
☐	L2	Reinl-Stephen$.in.	9
	DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=OR		
☐	L1	Reinl.in.	85

END OF SEARCH HISTORY

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NEWS	1		Web Page URLs for STN Seminar Schedule - N. America
NEWS	2		"Ask CAS" for self-help around the clock
NEWS	3	FEB 28	PATDPAFULL - New display fields provide for legal status data from INPADOC
NEWS	4	FEB 28	BABS - Current-awareness alerts (SDIs) available
NEWS	5	MAR 02	GBFULL: New full-text patent database on STN
NEWS	6	MAR 03	REGISTRY/ZREGISTRY - Sequence annotations enhanced
NEWS	7	MAR 03	MEDLINE file segment of TOXCENTER reloaded
NEWS	8	MAR 22	KOREAPAT now updated monthly; patent information enhanced
NEWS	9	MAR 22	Original IDE display format returns to REGISTRY/ZREGISTRY
NEWS	10	MAR 22	PATDPASPC - New patent database available
NEWS	11	MAR 22	REGISTRY/ZREGISTRY enhanced with experimental property tags
NEWS	12	APR 04	EPFULL enhanced with additional patent information and new fields
NEWS	13	APR 04	EMBASE - Database reloaded and enhanced
NEWS	14	APR 18	New CAS Information Use Policies available online
NEWS	15	APR 25	Patent searching, including current-awareness alerts (SDIs), based on application date in CA/CAplus and USPATFULL/USPAT2 may be affected by a change in filing date for U.S. applications.
NEWS	16	APR 28	Improved searching of U.S. Patent Classifications for U.S. patent records in CA/CAplus
NEWS	17	MAY 23	GBFULL enhanced with patent drawing images
NEWS	18	MAY 23	REGISTRY has been enhanced with source information from CHEMCATS
NEWS	19	JUN 06	The Analysis Edition of STN Express with Discover! (Version 8.0 for Windows) now available
NEWS	20	JUN 13	RUSSIAPAT: New full-text patent database on STN
NEWS	21	JUN 13	FRFULL enhanced with patent drawing images
NEWS	22	JUN 27	MARPAT displays enhanced with expanded G-group definitions and text labels
NEWS	23	JUL 01	MEDICONF removed from STN
NEWS	24	JUL 07	STN Patent Forums to be held in July 2005
NEWS	25	JUL 13	SCISEARCH reloaded
NEWS	26	JUL 20	Powerful new interactive analysis and visualization software, STN AnaVist, now available
NEWS	27	AUG 11	Derwent World Patents Index(R) web-based training during August
NEWS	28	AUG 11	STN AnaVist workshops to be held in North America

NEWS EXPRESS JUNE 13 CURRENT WINDOWS VERSION IS V8.0, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 13 JUNE 2005

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NEWS INTER General Internet Information

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 NEWS PHONE     Direct Dial and Telecommunication Network Access to STN
 NEWS WWW       CAS World Wide Web Site (general information)

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FILE 'HOME' ENTERED AT 09:08:39 ON 19 AUG 2005

=> linker (s) ?nuclotide (s) (variable or varying or varying) (s) (length or number)
THIS COMMAND NOT AVAILABLE IN THE CURRENT FILE
Some commands only work in certain files.  For example, the EXPAND
command can only be used to look at the index in a file which has an
index.  Enter "HELP COMMANDS" at an arrow prompt (=>) for a list of
commands which can be used in this file.

=> fil medline biosis caplus embase wpids
COST IN U.S. DOLLARS                            SINCE FILE      TOTAL
                                                   ENTRY    SESSION
FULL ESTIMATED COST                                 0.63       0.63

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FILE 'BIOSIS' ENTERED AT 09:10:09 ON 19 AUG 2005
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=> linker (s) ?nuclotide (s) (variable or varying or varying) (s) (length or number)
L1             0 LINKER (S) ?NUCLOTIDE (S) (VARIABLE OR VARYING OR VARYING) (S)
                 (LENGTH OR NUMBER)

=> linker (s) ?nucleotide (s) (variable or varying or varying) (s) (length or
number)
L2            23 LINKER (S) ?NUCLEOTIDE (S) (VARIABLE OR VARYING OR VARYING) (S)
                 (LENGTH OR NUMBER)

=> dup rem l2
PROCESSING COMPLETED FOR L2
L3             23 DUP REM L2 (0 DUPLICATES REMOVED)

=> t ti l3 1-23

L3   ANSWER 1 OF 23  WPIDS  COPYRIGHT 2005 THE THOMSON CORP on STN
TI   Preparing and amplifying a genome or a transcriptome comprises subjecting
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the molecule/primer mixture to a polymerase.

L3 ANSWER 2 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Use of a nematode polypeptide as an immunological adjuvant in preventing and/or treating allergies, autoimmune diseases, neurodegenerative disorders and cancer.

L3 ANSWER 3 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Identifying a desired region of a target nucleic acid, useful in detecting polymorphism and infectious microorganisms, by contacting the nucleic acid with oligomers coupled to particulate labels observable by microscopy.

L3 ANSWER 4 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Producing amplification target circles, by incubating binding guide conjugate that bind to analyte and half circle probes to promote ligation of half circle probes by guide oligonucleotide of conjugate that is complementary to probe.

L3 ANSWER 5 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Fragment complementation system for detecting immunoglobulin epitope, has first oligopeptide containing N-terminal fragment with C-terminal break-point, second oligopeptide containing C-terminal fragment with N-terminal break-point.

L3 ANSWER 6 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Directing the synthesis of a combinatorial library of oligomers, useful for permitting complex genetic analyses to be carried out, comprises using encoded carrier support systems.

L3 ANSWER 7 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Universal microarray for measuring gene expression, has substrate and several probes having universal sequence portion, short central variable wobble sequence portion and unique sequence portion, bound to substrate.

L3 ANSWER 8 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI New surface with an immobilized layer comprising probe molecules bound to the surface, useful for detecting or measuring the amount of one or more target molecules to identify potential therapeutics to treat diseases, such as cancer.

L3 ANSWER 9 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Library of expression vectors encoding protein complexes, useful for screening protein-protein or protein-DNA binding pairs, or for screening antibodies against a wide variety of targets, e.g. antigens associated with diseases.

L3 ANSWER 10 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Novel oligonucleotide linker or population of linkers for preparing polynucleotide libraries, comprises an oligonucleotide fixed portion and an oligonucleotide variable portion.

L3 ANSWER 11 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Screening libraries of tester proteins against protein, peptide or nucleic acid target(s) using a two-hybrid method in yeast, useful for generating recombinant human antibodies and screening for their affinity binding with target antigens.

L3 ANSWER 12 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
TI Oligonucleotides of variable length and sequence for use as linker regions for dual-domain or multi-domain molecules

L3 ANSWER 13 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

TI New bispecific molecules, useful for targeting multiple epitopes of pathogenic antigen, comprise binding domains that bind to pathogenic antigenic molecule and C3b-like receptor, and does not contain antibody to CR1.

L3 ANSWER 14 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Controlling cellular, organismal phenotypes comprises recombining conjoint polynucleotide segments to produce recombinant concatamer library which is expressed in cells and screened to identify cells with desired phenotype.

L3 ANSWER 15 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Novel probe sets with common universal linkers at one or both ends (WRAP probes) for gene expression arrays to provide global amplification of probe set and to provide common equivalent signaling regardless of length.

L3 ANSWER 16 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Detecting abnormal base-pairing, mutation in nucleic acid, or polymorphism in gene locus, comprises contacting nucleic acid with abnormal base-pairing and mutant nucleic acid repair enzyme, and detecting their binding.

L3 ANSWER 17 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Interaction-dependent enzyme association systems for detecting interactions between two or three polypeptides, especially in human therapeutics, diagnostics or prognostics, comprise circularly permutated proteins.

L3 ANSWER 18 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Analyzing a polynucleotide produced by amplifying cDNA or genomic DNA involves hybridizing terminus probes having constant and variable region to adapter-modified restriction fragment generated from the polynucleotide.

L3 ANSWER 19 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Novel fragment complementation system to identify interactions between polypeptides comprises fragment pairs having first and second members that reassemble into a marker protein which has a directly detectable signal.

L3 ANSWER 20 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Making immobilized nucleic acid molecule array comprises creating array nucleic acid capture activity spots to which an excess of nucleic acid molecules with excluded volume greater than spots are contacted.

L3 ANSWER 21 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Determining differential display of gene expression, useful for monitoring drug responses at the gene expression level and locating genes involved in a particular response, by comparisons between mono-length cRNA libraries.

L3 ANSWER 22 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
TI Analysis of polynucleotides using hybridization assays, useful for providing nucleotide sequences or relative concentrations which can be used in the prediction, diagnosis and treatment of diseases.

L3 ANSWER 23 OF 23 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI SYNTHESIS AND CHARACTERIZATION OF NUCLEOSIDE PEPTIDES TOWARD CHEMICAL RNASES 1.

=> d ibib abs l3 1-23

L3 ANSWER 1 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER: 2004-677550 [66] WPIDS
DOC. NO. CPI: C2004-241513
TITLE: Preparing and amplifying a genome or a transcriptome comprises subjecting the molecule/primer mixture to a polymerase.
DERWENT CLASS: B04 D16
INVENTOR(S): BRUENING, E; KAMBEROV, E; KURIHARA, T; MAKAROV, V L; PINTER, J H; SLEPTSOVA, I; SUN, T; PINTER, J
PATENT ASSIGNEE(S): (BRUE-I) BRUENING E; (KAMB-I) KAMBEROV E; (KURI-I) KURIHARA T; (MAKA-I) MAKAROV V L; (PINT-I) PINTER J H; (SLEP-I) SLEPTSOVA I; (SUNT-I) SUN T; (RUBI-N) RUBICON GENOMICS INC
COUNTRY COUNT: 108
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2004081225	A2	20040923	(200466)*	EN	208

RW: AT BE BG BW CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE LS LU MC MW MZ NL OA PL PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BW BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE EG ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NA NI NO NZ OM PG PH PL PT RO RU SC SD SE SG SK SL SY TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW

US 2004209298	A1	20041021	(200470)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2004081225	A2	WO 2004-US6983	20040308
US 2004209298	A1 Provisional	US 2003-453060P	20030307
		US 2004-795667	20040308

PRIORITY APPLN. INFO: US 2003-453060P 20030307; US 2004-795667 20040308
AN 2004-677550 [66] WPIDS
AB WO2004081225 A UPAB: 20041015
NOVELTY - Preparing and amplifying a genome, a transcriptome, or both, or a nucleic acid, e.g. DNA or RNA molecule or a DNA molecule generated from at least one mRNA molecule, comprises subjecting the DNA molecule/primer mixture or the RNA molecule/primer mixture or the ssDNA molecule/primer mixture to a polymerase, under conditions where the subjecting steps generate molecules including all or part of the constant region at each end.

DETAILED DESCRIPTION - Preparing and amplifying a genome, a transcriptome, or both, or a nucleic acid, e.g. DNA or RNA molecule or a DNA molecule generated from at least one mRNA molecule, comprises:

(a) obtaining at least one nucleic acid molecule or at least one double stranded or single stranded DNA molecule or at least one RNA molecule or a cDNA molecule from the mRNA molecule or both DNA and RNA;

(b) subjecting the double stranded DNA molecule to heat or optionally heating the RNA molecule or modifying the cDNA molecule to produce at least one single stranded DNA or RNA or ssDNA molecule;

(c) subjecting the single stranded DNA or RNA or ssDNA molecule to primers to form a DNA molecule/primer mixture or RNA molecule/primer mixture or ssDNA molecule/primer mixture, where the primers comprise nucleic acid sequence that is substantially non-self-complementary and substantially non-complementary to other primers, and where the sequence comprises in a 5' to 3' orientation a constant region and a variable

region;

(d) subjecting the DNA molecule/primer mixture or the RNA molecule/primer mixture or the ssDNA molecule/primer mixture to a polymerase, under conditions where the subjecting steps generate molecules including all or part of the constant region at each end; and

(e) amplifying DNA molecules through PCR, the reaction utilizing a primer complementary to the constant region.

INDEPENDENT CLAIMS are also included for:

(1) a method of obtaining a total nucleic acid from a sample comprising a mixture of DNA and RNA;

(2) a method of differentially obtaining DNA or RNA, respectively, from a sample comprising a mixture of DNA and RNA;

(3) polynucleotides comprising nucleic acid sequences that are substantially non-self-complementary and substantially non-complementary to other polynucleotides;

(4) a kit comprising polynucleotides of (3) dispersed in a container;

(5) a method of immobilizing an amplified genome, transcriptome, or both;

(6) dsDNA molecules comprising genomic DNA, when the molecules are denatured to produce first and second strand molecules, each of which comprises a first and second end region at the respective ends of the first and second strand molecules, and each of the first and second end regions of the first and second molecule comprise nucleic acid sequence that is substantially non-self-complementary to sequence in the first and second end regions in the first and second molecule; and

(7) a method of sequencing a genome from a limited source of material.

USE - The methods and kits are useful for preparing and amplifying a genome, a transcriptome, or both, or a nucleic acid, e.g. DNA or RNA molecule or a DNA molecule generated from at least one mRNA molecule.

Dwg.0/51

L3 ANSWER 2 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER: 2004-562092 [54] WPIDS

DOC. NO. CPI: C2004-205481

TITLE: Use of a nematode polypeptide as an immunological adjuvant in preventing and/or treating allergies, autoimmune diseases, neurodegenerative disorders and cancer.

DERWENT CLASS: B04 D16

INVENTOR(S): HEATH, A; LANG, P

PATENT ASSIGNEE(S): (ADJU-N) ADJUVANTIX LTD

COUNTRY COUNT: 108

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2004064864	A1	20040805	(200454)*	EN	94

RW: AT BE BG BW CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE LS LU MC MW MZ NL OA PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BW BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE EG ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NA NI NO NZ OM PG PH PL PT RO RU SC SD SE SG SK SL SY TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2004064864	A1	WO 2004-GB149	20040121

PRIORITY APPLN. INFO: GB 2003-1433 20030122
AN 2004-562092 [54] WPIDS
AB WO2004064864 A UPAB: 20040823
NOVELTY - Use of a polypeptide as an immunological adjuvant, where the polypeptide comprises an amino acid motif consisting of the amino acid residues RXK/RR and/or an amino motif consisting of the amino acid residues RXFR.

DETAILED DESCRIPTION - The polypeptide has an amino acid motif with residues RXK/RR, where

R = arginine; X = any amino acid residue; and K = lysine,

and/or residues RXFR, where

F = phenylalanine,

and further where the motif is preceded by a cysteine amino acid residue about 7-9 residues amino terminal to the motif which polypeptide can be modified by addition, deletion, or substitution of at least one amino acid residue.

INDEPENDENT CLAIMS are also included for:

(1) a vaccine composition comprising at least one polypeptide as cited above, and at least one antigen to which an immune response is desired;

(2) a nucleic acid molecule which encodes conjugate where the conjugate comprises an antigenic polypeptide translationally fused to a nematode derived ladder protein in which an RX(K/R)R or RRFR motif is preceded 7, 8 or 9 residues upstream by a cysteine residue;

(3) a vector comprising a nucleic acid molecule of (2), where the nucleic acid molecule is operably linked to a promoter which controls the expression of the conjugate;

(4) a vaccine comprising a nucleic acid of (2) or a vector of (3);

(5) immunize an animal to an antigen, comprising administering a nucleic acid of (2) or a vector of (3) to stimulate an immune response to the antigen;

(6) an antibody obtainable by the method of (5);

(7) preparing a hybridoma cell-line producing monoclonal antibodies, comprising immunizing an immunocompetent mammal with a conjugate, composition, nucleic acid or vector as cited above, fusing lymphocytes of the immunized immunocompetent mammal with myeloma cells to form hybridoma cells, screening monoclonal antibodies produced by the hybridoma cells for binding activity to the antigen of the conjugate, culturing the hybridoma cells to proliferate and/or to secrete the monoclonal antibody, and recovering the monoclonal antibody from the culture supernatant; and

(8) a hybridoma cell-line obtainable by the method of (7).

ACTIVITY - Antiallergic; Immunosuppressive; Neuroprotective; Nootropic; Cytostatic.

No biological data given.

MECHANISM OF ACTION - Vaccine.

USE - The polypeptide is encoded by a nucleic acid molecule where there is at least one amino acid motif of the sequence RX(K/R)R, where

R = arginine; X = any amino acid; K/R = lysine or arginine; and R = arginine;

or RXFR motif, where

F = phenylalanine,

preceded by a cysteine residue 7, 8, or 9 residues N-terminal of the RX(KTR)R or RRFR amino acid motif. The polypeptide is encoded by a nematode nucleic acid molecule (all claimed). They are also useful in preventing and/or treating allergies, autoimmune diseases, neurodegenerative disorders and cancer.

Dwg.0/0

L3 ANSWER 3 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2004-420635 [39] WPIDS
DOC. NO. CPI: C2004-157982

TITLE: Identifying a desired region of a target nucleic acid, useful in detecting polymorphism and infectious microorganisms, by contacting the nucleic acid with oligomers coupled to particulate labels observable by microscopy.

DERWENT CLASS: B04 D16

INVENTOR(S): CROMER, R; KAUVAR, L M; STRANDH, M

PATENT ASSIGNEE(S): (CROM-I) CROMER R; (KAUV-I) KAUVAR L M; (STRA-I) STRANDH M; (TREL-N) TRELLIS BIOSCIENCE INC

COUNTRY COUNT: 107

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2004046372	A2	20040603	(200439)*	EN	34
RW: AT BE BG BW CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE LS LU MC MW MZ NL OA PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE EG ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NI NO NZ OM PG PH PL PT RO RU SC SD SE SG SK SL SY TJ TM TN TR TT TZ UA UG UZ VC VN YU ZA ZM ZW					
US 2004185467	A1	20040923	(200463)		
AU 2003291045	A1	20040615	(200470)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2004046372	A2	WO 2003-US36801	20031113
US 2004185467	A1 Provisional	US 2002-426782P	20021114
		US 2003-713632	20031113
AU 2003291045	A1	AU 2003-291045	20031113

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2003291045	A1 Based on	WO 2004046372

PRIORITY APPLN. INFO: US 2002-426782P 20021114; US 2003-713632 20031113

AN 2004-420635 [39] WPIDS

AB WO2004046372 A UPAB: 20040621

NOVELTY - Identifying a desired region of a target nucleic acid to be targeted for observation comprises contacting the nucleic acid with identification probes comprising oligomers coupled to particulate labels observable by microscopy.

DETAILED DESCRIPTION - Identifying a desired region of a target nucleic acid to be targeted for observation comprises contacting the nucleic acid with first and second identification probes, which probes comprise first and second oligomers specific for the upstream and downstream sequences bracketing the region respectively, where the first and second oligomers are coupled to a first and second particulate label, respectively, and where the particulate labels are observable by microscopy.

INDEPENDENT CLAIMS are also included for:

(1) detecting the presence of a target nucleic acid of known sequence;

(2) a composition comprising a target nucleic acid comprising a region bracketed by sequences formed by binding to a first and a second oligomer described above;

(3) assessing the length of a target nucleic acid segment that is composed of a variable number of repeated sequences; and

(4) detecting a single nucleotide polymorphism (SNP) at a base that is included in a restriction site haploid.

USE - The methods and kits are useful in identifying a desired region of a target nucleic acid to be targeted for observation, in detecting SNPs and infectious microorganisms and in diagnosing a disease, e.g. Huntington's disease.

Dwg.0/3

L3 ANSWER 4 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2005-030157 [03] WPIDS
DOC. NO. CPI: C2005-009554
TITLE: Producing amplification target circles, by incubating binding guide conjugate that bind to analyte and half circle probes to promote ligation of half circle probes by guide oligonucleotide of conjugate that is complementary to probe.
DERWENT CLASS: A18 A28 A96 B04 D16
INVENTOR(S): FEAVER, W J; MULLENIX, M
PATENT ASSIGNEE(S): (FEAV-I) FEAVER W J; (MULL-I) MULLENIX M
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 2004248103	A1	20041209	(200503)*		75

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 2004248103	A1	US 2003-454946	20030604

PRIORITY APPLN. INFO: US 2003-454946 20030604
AN 2005-030157 [03] WPIDS
AB US2004248103 A UPAB: 20050112

NOVELTY - Producing amplification target circles (ATC), by incubating analyte and binding guide conjugates (BC) having specific binding molecule (B1) that binds with analyte, and guide oligonucleotide (O1), for interaction of (B1) and analytes, incubating BC and half circle probes (P1) having single stranded DNA comprising two guide complement portions, for hybridizing (O1) and (P1), incubating the BC and (P1) to ligate (P1) and produce ATC, is new.

DETAILED DESCRIPTION - Producing (M1) amplification target circles (ATC), involves

(a) bringing into contact analyte samples and binding guide conjugates (BC), where each BC comprises a specific binding molecule and a guide oligonucleotide, where each specific binding molecule interacts with an analyte in the analyte sample, and incubating the analyte samples and BC under conditions that promote interaction;

(b) bringing into contact the BC and half circle probes, where each half circle probe comprises a single stranded DNA molecule with two guide complement portions, where guide complement portion is complementary to one of the guide oligonucleotides, and incubating the BC and the half circle probes under conditions that promote hybridization; and

(c) incubating the BC and half circle probes under conditions that promotes ligation of half circle probes.

Alternatively, the method involves:

(i) performing steps (a), and (b), where each guide oligonucleotide is complementary to one of the guide complement portions of both half

circle probes in a pair of half circle probes, where the guide complement portions of the same half circle probe are complementary to two different guide oligonucleotides, where the two different guide oligonucleotides that each are complementary to a different one of the guide complement portions of the same half circle probe constitute a pair of guide oligonucleotides, where the BC that comprise the guide oligonucleotides in a pair of guide oligonucleotides constitute a pair of BC, where one guide complement portion of each half circle probe in a pair of half circle probes is complementary to one of the guide oligonucleotides in a pair of guide oligonucleotides and the other guide complement portion of each half circle probe in the pair of half circle probes is complementary to the other guide oligonucleotide in the pair of guide oligonucleotides, where both half circle probes in a pair of half circle probes are hybridized to both guide oligonucleotides in a pair of guide oligonucleotides;

(ii) incubating the BC and the half circle probes under conditions that promote hybridization; and

(iii) incubating the BC and half circle probes under conditions that promote ligation of half circle probes in pairs of half circle probes to each other.

INDEPENDENT CLAIMS are also included for:

(1) forming (M2) tandem sequence DNA, by:

(a) bringing into contact analyte samples and arrays, where each array comprises analyte capture agents, and/or accessory molecules, where each analyte capture agent interacts with an analyte directly or indirectly;

(b) bringing into contact the arrays or analyte samples and BC, where each BC comprises a specific binding molecule and a guide oligonucleotide, where each specific binding molecule interacts with an analyte in the analyte sample, and incubating the analyte samples and the BC under conditions that promote interaction;

(c) bringing into contact the BC and half circle probes, where each half circle probe comprises a single-stranded DNA molecule comprising two guide complement portions, where each guide complement portion is complementary to at least one of the guide oligonucleotides, and incubating the BC and the half circle probes under conditions that promote hybridization;

(d) incubating the BC and half circle probes under conditions that promote ligation of half circle probes to each other, thus producing ATC; and

(e) incubating the ATC under conditions that promote replication of the ATC, where replication of the ATC results in the formation of tandem sequence DNA;

(2) forming (M3) tandem sequence DNA, by:

(a) treating analyte samples so that one or more analytes are modified;

(b) bringing into contact the analyte samples and BC, where each BC comprises a specific binding molecule and a guide oligonucleotide, where each specific binding molecule interacts with an analyte in the analyte sample, and incubating the analyte samples and the BC under conditions that promote interaction;

(c) bringing into contact the BC and half circle probes, where each half circle probe comprises a single-stranded DNA molecule comprising two guide complement portions, where each guide complement portion is complementary to at least one of the guide oligonucleotides, and incubating the BC and the half circle probes under conditions that promote hybridization between the guide oligonucleotides and the half circle probes;

(d) incubating the BC and half circle probes under conditions that promote ligation of half circle probes to each other, thus producing ATC; and

(e) incubating the ATC under conditions that promote replication of the ATC, where replication of the ATC results in the formation of tandem

sequence DNA; or

(3) forming (M4) tandem sequence DNA, by:

(a) bringing into contact analyte samples and binding half circle conjugates, where each binding half circle conjugate comprises a specific binding molecule and a half circle probe, where each specific binding molecule interacts with an analyte in the analyte sample, and where each half circle probe comprises a single-stranded DNA molecule comprising two guide complement portions, and incubating the analyte samples and the conjugates;

(b) bringing into contact the binding half circle conjugates and one or more guide oligonucleotides, where each guide oligonucleotide is complementary to at least one of the guide complement portions of the half circle probes, and incubating the binding half circle conjugates and the guide oligonucleotides under conditions that promote hybridization;

(c) incubating the binding half circle conjugates and guide oligonucleotides under conditions that promote ligation of half circle probes to each other, thus producing ATC and

(d) incubating the ATC under conditions that promote replication of the ATC, where replication of the ATC results in the formation of tandem sequence DNA; and

(4) a kit for performing (M1) and (M2), comprising several BC, and several of half circle probes.

USE - (M1) is useful for producing amplification target circles. (M1) is useful for formation of tandem sequence DNA (claimed). (M1) is useful for producing ATC that are used to form long strands (tandem sequence DNA) with tandem repeats of sequence complementary to the circular template, by proximity mediated rolling circuit amplification. (M1) is useful for detection of analyte, analysis of nucleic acid present in cells, disease detection, mutation detection, gene discovery, gene mapping, and agricultural research.

Dwg.0/14

L3 ANSWER 5 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER: 2004-203222 [19] WPIDS
CROSS REFERENCE: 2001-032034 [04]; 2001-451857 [48]
DOC. NO. NON-CPI: N2004-161667
DOC. NO. CPI: C2004-080008
TITLE: Fragment complementation system for detecting immunoglobulin epitope, has first oligopeptide containing N-terminal fragment with C-terminal break-point, second oligopeptide containing C-terminal fragment with N-terminal break-point.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): BALINT, R F; HER, J
PATENT ASSIGNEE(S): (KALO-N) KALOBIOS INC
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 2004038317	A1	20040226	(200419)*		47

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
US 2004038317	A1	Provisional	US 1999-124339P	19990315
		Provisional	US 1999-135926P	19990525
		Provisional	US 2000-175968P	20000113
		Cont of	US 2000-526106	20000315
			US 2003-668778	20030922

PRIORITY APPLN. INFO: US 2003-668778 20030922; US
1999-124339P 19990315; US
1999-135926P 19990525; US
2000-175968P 20000113; US
2000-526106 20000315

AN 2004-203222 [19] WPIDS

CR 2001-032034 [04]; 2001-451857 [48]

AB US2004038317 A UPAB: 20040527

NOVELTY - A fragment complementation system (I) comprising a first oligopeptide having an N-terminal fragment with a C-terminal break-point, and a second oligopeptide having a C-terminal fragment with a N-terminal break-point, where the N-terminal fragment and the C-terminal fragment each are derived from a marker protein and reassemble to form a functionally reconstituted marker protein.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) identifying (M1) a functional fragment pair in a protein involves preparing a fragments of a marker protein where each fragment has a break-point terminus within a solvent exposed loop of the marker protein, where the N or C terminal residue of each C or N terminal fragment, respectively, constitutes the break-point terminus, to obtain a marker fragment library, expressing in several host cells, members of the marker fragment library, isolating host cells expressing the marker protein as indicative of a cell containing a first member and a second member of a fragment pair which have formed a functionally reconstituted the marker protein, identifying the functional fragment pair;

(2) an expression cassette (II) comprising as operably linked components in the direction of transcription nucleotide sequences encoding for a promoter functional in a host cell, a polypeptide interactor domain, a flexible polypeptide linker, and a C-terminal fragment of a marker protein that provides for a selectable phenotype and/or an N-terminal fragment of a protein that provides for a selectable phenotype; and

(3) host cell (III) comprising (II) as first and second expression cassette.

USE - (I) is useful for selecting simultaneous incorporation of multiple genetic elements into a host cell, and isolating cells resistant to the antibiotic. (I) is useful for activating beta -lactam derivative of an anti-tumor compound in a host, which involves administering to the host a first oligopeptide and a second oligopeptide, the first oligopeptide comprising an N-terminal fragment of beta -lactamase, a flexible polypeptide linker and a first single chain Fv fragment against an epitope of a tumor protein, the second oligopeptide comprises a second single chain Fv against a second non-overlapping epitope of the tumor protein, a flexible polypeptide linker and a C-terminal fragment of beta -lactamase, where the single chain Fv fragments bind to the epitopes resulting in the functional reconstitution of beta -lactamase, and administering the beta -lactam derivative of the anti-tumor compound to the host, activating the derivative by the reconstituted beta -lactamase near the tumor protein. (M1) is useful for identifying a second oligopeptide to which a first oligopeptide binds, which involves co-expressing in several host cells the first oligopeptide and second oligopeptide, where the second oligopeptide is encoded by a member of a library, each as a fusion protein with a first member and a second member of a fragment pair of a marker protein, respectively, obtained by (M1), where binding of the first oligopeptide to the second oligopeptide results in the functional reassembly of the marker protein, isolating host cells expressing the marker protein as indicative of a cell containing a first oligopeptide and a second oligopeptide which have interacted, and sequencing plasmids containing expression cassettes coding for the fusion proteins, identifying the second oligopeptide to which the first oligopeptide binds, where first oligopeptide and the second oligopeptide are extracellular proteins. The cell surface molecule

is CD40. The phosphorylation-regulated signal transducer protein is a tyrosine kinase. (M1) is useful for monitoring the occurrence of protein-protein interactions in a sample, which involves co-expressing in a host cell a first oligopeptide member of a first cellular library and a second oligopeptide member of a second cellular library, each as a fusion protein with a first member and a second member of a fragment pair of a marker protein, respectively obtained (M1), where binding of the first oligopeptide to the second oligopeptide results in the functional reassembly of the marker protein, isolating host cells expressing the marker protein as indicative of a cell containing a first member and a second member of a fragment pair which have functionally reconstituted the marker protein, sequencing plasmids containing expression cassettes coding for the fusion proteins, monitoring protein-protein interactions. (M1) is useful for identifying oligopeptide interactions between two different proteomes, which involves co-expressing in a host cell a first oligopeptide member of a first cellular library and a second oligopeptide member of a second cellular library, obtained by (M1), sequencing plasmids containing expression cassettes coding for the fusion proteins, identifying the oligopeptide interactions between two different proteomes, where cellular library is from a tumor cell or an immune cell. (I) or (II) is useful for identifying epitopes that bind to an immunoglobulin variable region, which involves co-expressing from plasmids comprising (II) in a host cell a first oligopeptide and a second oligopeptide, the first oligopeptide comprising an N-terminal fragment of beta -lactamase fused operably in frame through a cysteine residue or a stabilizing tripeptide to a flexible polypeptide linker and a first interactor domain comprised of a randomly encoded peptide inserted into the active site of thioredoxin, and the second oligopeptide comprising a second interactor domain comprised of a single chain Fv fragment or an antibody lights chain variable region and a flexible polypeptide linker fused operably in frame through a cysteine residue or a stabilizing tripeptide to a C-terminal fragment of beta -lactamase, where the binding of the first interactor domain with the second interactor domain results in the functional reconstitution of the beta -lactamase, isolating host cells resistant to ampicillin, sequencing plasmids containing expression cassettes coding for the first and second oligopeptides, identifying epitopes that bind to the immunoglobulin variable regions. (I) or (II) is useful for identifying interaction between and extra cellular domain of a transmembrane protein and a polypeptide, where the transmembrane protein is an immune cell protein, preferably CD40. (I) or (II) is useful for high-throughput identification of compound that inhibit phosphorylation-regulated cell signal transducers (all claimed).

ADVANTAGE - (I) efficiently detects multiple interaction between extracellular and intracellular protein with high throughput format.

DESCRIPTION OF DRAWING(S) - The figure shows the schematic representation of vectors and strategy for the expression of heterologous proteins as fusions to the alpha 197 and omega 198 fragments of TEM-1 beta -lactamase for interaction-dependent beta -lactamase activation by fragment complementation.

Dwg.6/11

L3 ANSWER 6 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER:	2003-430580 [40] WPIDS
DOC. NO. NON-CPI:	N2003-343694
DOC. NO. CPI:	C2003-113945
TITLE:	Directing the synthesis of a combinatorial library of oligomers, useful for permitting complex genetic analyses to be carried out, comprises using encoded carrier support systems.
DERWENT CLASS:	B04 D16 T01
INVENTOR(S):	BATTERSBY, B J; JOHNSTON, A; MILLER, C R; TRAU, M; WAY, J C

PATENT ASSIGNEE(S): (BATT-I) BATTERSBY B J; (JOHN-I) JOHNSTON A; (MILL-I) MILLER C R; (TRAU-I) TRAU M; (WAYJ-I) WAY J C; (NANO-N) NANOMICS BIOSYSTEMS PTY LTD
COUNTRY COUNT: 102
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2003038558	A2	20030508	(200340)*	EN	79
RW: AT BE BG CH CY CZ DE DK EA EE ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SK SL SZ TR TZ UG ZM ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW					
US 2003182068	A1	20030925	(200364)		
EP 1448789	A2	20040825	(200456)	EN	
R: AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI SK TR					
AU 2002357677	A1	20030512	(200464)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2003038558	A2	WO 2002-US34775	20021030
US 2003182068	A1 Provisional	US 2001-330759P	20011030
		US 2002-283741	20021030
EP 1448789	A2	EP 2002-792214	20021030
		WO 2002-US34775	20021030
AU 2002357677	A1	AU 2002-357677	20021030

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1448789	A2 Based on	WO 2003038558
AU 2002357677	A1 Based on	WO 2003038558

PRIORITY APPLN. INFO: US 2001-330759P 20011030; US 2002-283741 20021030
AN 2003-430580 [40] WPIDS
AB WO2003038558 A UPAB: 20030624
NOVELTY - Directing (M) the synthesis of a combinatorial library of oligomers comprising using encoded carrier support systems, is new.

DETAILED DESCRIPTION - M comprises:

(a) prior to coupling, assigning a predetermined oligomer sequence to each of a plurality of carriers having a distinguishable feature;

(b) sorting the plurality of carriers into a plurality of reaction vessels, where the vessel into which each carrier is sorted is determined by the oligomer assigned to each carrier based on the distinguishable feature, and where each carrier is sorted independently of the other carriers;

(c) performing a reaction to couple a chemical moiety to each carrier in each vessel, where the chemical moiety is the same or different in different vessels; and

(d) repeating steps (b) and (c) at least once, where in each step, a subsequent chemical group is coupled to the previously added chemical group to produce a plurality of oligomers, thus, directing the synthesis of a combinatorial library of oligomers.

INDEPENDENT CLAIMS are also included for:

(1) a library of encoded carriers, the library comprising a plurality of carriers where each of the carriers comprises a unique distinguishing feature and a unique oligomer bound to the carrier;

(2) a device for sorting carriers, comprising a sorter having a flow path that splits into at least two branches into which carriers can be sorted; one or more detectors capable of detecting the carriers in the flow path, where the one or more detectors are disposed to detect the carriers prior to passing into one of the branches; and a computer that determines the branch into which each carrier is sorted based on one or more signals from each carrier obtained from the detectors;

(3) a sort computer, comprising an interface that is capable of receiving data that encodes a distinguishable feature of a carrier as it is passed through the above sorting device; one or more memories that store the number of carriers; a controller that is capable of controlling the sorting device to sort the carrier into one of the branches; and a sorting selector that determines into which branch the carrier is sorted based on the number of carriers stored in the memories;

(4) discontinuously sorting carriers;

(5) identifying an oligomer that binds to a species;

(6) synthesizing a library of oligonucleotides or a combinatorial library;

(7) isolating a subpopulation of carriers from a diverse population of carriers;

(8) making a non-combinatorial library; and

(9) a machine readable data memory comprising an oligomer encoding database that includes a list of sequences of chemical moieties that form an oligomer, with each chemical group associated with at least one combination of particular values of bead parameters at a given step in a synthesis, and where particular values of beads are accessible by machine to provide identification data for a synthesis and where parameter values of beads indicate that a bead should be sorted in a given direction.

USE - M is useful in synthesizing chemical libraries that are sufficiently large, for example, to permit complex genetic analyses to be carried out.

Dwg.0/58

L3 ANSWER 7 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER: 2003-111992 [10] WPIDS
DOC. NO. NON-CPI: N2003-089134
DOC. NO. CPI: C2003-028684
TITLE: Universal microarray for measuring gene expression, has substrate and several probes having universal sequence portion, short central variable wobble sequence portion and unique sequence portion, bound to substrate.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): FAGAN, J
PATENT ASSIGNEE(S): (FAGA-I) FAGAN J; (GENE-N) GENETIC ID INC
COUNTRY COUNT: 100
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2002090599	A1	20021114	(200310)*	EN	60
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG UZ VN YU ZA ZM ZW					
US 2003003484	A1	20030102	(200310)		
AU 2002309704	A1	20021118	(200452)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002090599	A1	WO 2002-US14750	20020509
US 2003003484	A1 Provisional	US 2001-289864P	20010509
		US 2002-143522	20020509
AU 2002309704	A1	AU 2002-309704	20020509

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2002309704	A1 Based on	WO 2002090599

PRIORITY APPLN. INFO: US 2001-289864P 20010509; US 2002-143522 20020509

AN 2003-111992 [10] WPIDS

AB WO 200290599 A UPAB: 20030211

NOVELTY - A universal microarray (I) comprising a solid substrate and several oligonucleotide probes bound to several spots on the substrate, is new.

DETAILED DESCRIPTION - A universal microarray (I) comprises a solid substrate and several oligonucleotide probes bound to several spots on the substrate, where the probes have the form B-C-D.

B = a unique z-mer comprising 5-8 nucleotide bases such that all 4z permutations of A, G, C and T are represented in several oligonucleotide probes and only one 4z permutations is present in each spot;

C = a variable x-mer comprising at least 1 nucleotide base so that all 4x permutations of A, G, C and T are represented in the oligonucleotide probes and all 4x permutations are present in every spot in equal concentrations; and

D = a universal n-mer comprising 5-8 nucleotide bases that is the same for every probe.

INDEPENDENT CLAIMS are also included for the following:

(1) a set of primers (II) having the form F-G, where F and G are the same length as and complementary to the universal n-mer and variable x-mers, respectively, of the probes of (I) so that all possible 4x permutations of F-G are represented in the set of primers; and

(2) a kit for determining or measuring relative gene expression between 2 or more test mixtures, comprising (I) and (II).

USE - (I) and (II) are useful for determining relative gene expression between 2 or more test mixtures. The method comprises separately contacting each of the populations of mRNA derived from each of the 2 or more test mixtures to each of the members of (II) to generate 4x primed mRNA populations for each test mixture, segregating the primed mRNA populations into one or more subsets of mRNA populations, and separately synthesizing cDNA populations from each of the primed mRNA populations in each subset of mRNA populations by reverse transcription. Each of the synthesized cDNA populations is recovered with the primers attached to it to obtain one or more cDNA subsets corresponding to the subsets of the primed mRNA populations from which they were derived, and each member of a subset of cDNA populations is differentially labeled. The differentially labeled members are contacted with (I) for each subset of cDNA populations, so that portions C and D of the probes of the microarray are complementary to portions G and F, respectively, of the primer set used to synthesize the cDNA populations, and each spot is contacted with all of the differentially labeled members of a subset of cDNA populations under conditions such that complementary cDNA and probe sequences hybridize. The members of the cDNA subset are pooled prior to contacting one or more spots on the microarray with the labeled members. The steps are repeated for each subset of cDNA populations such that each subset of cDNA

populations contacts a microarray not previously contacted with any other subset of cDNA populations and the signal generated from every spot on every array is detected. The relative gene expression of the test mixtures is then determined by comparing the signal from a spot on one array to the corresponding spot on every other array where the probes on corresponding spots comprise the same unique z-mer, or comparing the signal from different labels on a single spot. The amount of cDNA in each cDNA population is normalized relative to every other population prior to contacting with the microarray. After the step of recovering, the concentration of cDNA in each of the labeled cDNA populations is normalized such that the total amount of cDNA contacting the spots in the microarray is about equal for each of the labeled cDNA populations. The step of labeling occurs during synthesis of the cDNA populations. At least one of the dNTPs used for reverse transcription is present in a form that terminates cDNA synthesis. The dNTP that terminates cDNA population synthesis is labeled, and the cDNA is terminated at 50-100 bases. At least one of the dNTPs used for reverse transcription is present in labeled and unlabeled forms. The cDNA is labeled after its synthesis, with a label such as dyes (e.g. fluorescent, chemiluminescent, bioluminescent, electroluminescent), particles (e.g. glass, silica, polymer, metal or semiconductor particles), and radioactive substances. The method further comprises providing a second and third set of microarrays and a second and third set of complementary primers, where the complementary universal n-mers of the probes and primers in the second set are different from the universal n-mers of the first set, and those of third set are different from the first and second sets, and performing all the steps using the second and third set of microarrays and primers. The probes and primers in the second set have a different GC content than the probes and primers in the first set. (All claimed.) The universal microarray system finds use in a number of different applications including examining effects of disease states and physiological states of specific cell and tissue types and determining the effects of a drug or other compound on gene expression. (II) is useful in the synthesis of oligonucleotides that are complementary to the probes on the universal microarray.

ADVANTAGE - The microarray system is a simple, cost-effective, universal method for determining and/or quantifying differences in nucleic acid levels between two or more test mixtures without prior knowledge of the sequence of the nucleic acids of interest.

Dwg.0/7

L3 ANSWER 8 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER: 2003-075568 [07] WPIDS
DOC. NO. NON-CPI: N2003-058500
DOC. NO. CPI: C2003-019631
TITLE: New surface with an immobilized layer comprising probe molecules bound to the surface, useful for detecting or measuring the amount of one or more target molecules to identify potential therapeutics to treat diseases, such as cancer.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): KRULL, U J
PATENT ASSIGNEE(S): (KRUL-I) KRULL U J
COUNTRY COUNT: 98
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2002084285	A2	20021024	(200307)*	EN	56

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR

LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE
SG SI SK SL TJ TM TN TR TT TZ UA UG UZ VN YU ZA ZM ZW
US 2003055233 A1 20030320 (200323)
AU 2002245988 A1 20021028 (200433)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002084285	A2	WO 2002-CA543	20020418
US 2003055233	A1 Provisional	US 2001-284715P	20010418
		US 2002-126504	20020418
AU 2002245988	A1	AU 2002-245988	20020418

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2002245988	A1 Based on	WO 2002084285

PRIORITY APPLN. INFO: US 2001-284715P 20010418; US 2002-126504 20020418
AN 2003-075568 [07] WPIDS
AB WO 200284285 A UPAB: 20030129
NOVELTY - A surface with an immobilized layer (IL) comprising probe molecules bound to the surface, where the IL has at least one spatially distributed gradient of probe molecules, and the gradient is formed by selectively varying a physical, structural or functional property of probe molecules bound to the surface as a function of the location on the surface to which the probe molecules are bound, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a biosensor for detection of one or more target molecules, comprising the surface;

(2) separating two or more molecules in a sample;

(3) detecting one or more target molecules in a sample;

(4) measuring the amount of one or more target molecules in the sample;

(5) making spatial distributed surface charge gradients on a surface;

(6) preparing a surface having a density gradient of bound probe molecules; and

(7) a kit for conducting an assay for detecting the amount of one or more target molecules in a sample comprising one or more of the surfaces.

USE - The surface, biosensor and kits are useful for detecting or measuring the amount of one or more target molecules (claimed). The surface is also useful for determining the selectivity to targets. The methods are useful for detecting and measuring genetic disorders and diseases such as cancer, and to identify potential therapeutics to treat such diseases. They are all useful in determining the association of compounds with nucleic acids or nucleic acid analogs.

ADVANTAGE - The advantages of the invention includes reversibility of chemistry, the ability to use tethered markers and/or mixed markers, and the use of calibration and referencing signals that appear concurrently with the analytical signal.

DESCRIPTION OF DRAWING(S) - The figure depicts a surface showing a two-dimensional gradient, where in one direction the density of probe molecules is varied, and in other dimension, the length of the immobilized sequence is varied.

Dwg.1/3

L3 ANSWER 9 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2002-590677 [63] WPIDS

DOC. NO. NON-CPI: N2002-468706
DOC. NO. CPI: C2002-167131
TITLE: Library of expression vectors encoding protein complexes, useful for screening protein-protein or protein-DNA binding pairs, or for screening antibodies against a wide variety of targets, e.g. antigens associated with diseases.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): HUA, S B; LIN, Y; SHERIDAN, J; ZHU, L
PATENT ASSIGNEE(S): (HUAS-I) HUA S B; (LINY-I) LIN Y; (SHER-I) SHERIDAN J; (ZHUL-I) ZHU L; (GENE-N) GENETASTIX CORP
COUNTRY COUNT: 98
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2002055718	A2	20020718	(200263)*	EN	202
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
US 6610472	B1	20030826	(200357)		
US 2003219817	A1	20031127	(200378)		
AU 2002245196	A1	20020724	(200427)		
US 2005123996	A1	20050609	(200538)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002055718	A2	WO 2001-US51044	20011031
US 6610472	B1	US 2000-703399	20001031
US 2003219817	A1 Div ex	US 2000-703399	20001031
		US 2003-423495	20030424
AU 2002245196	A1	AU 2002-245196	20011031
US 2005123996	A1 Div ex	US 2000-703399	20001031
	Cont of	US 2003-423495	20030424
		US 2004-947610	20040921

FILING DETAILS:

PATENT NO	KIND	PATENT NO
US 2003219817	A1 Div ex	US 6610472
AU 2002245196	A1 Based on	WO 2002055718
US 2005123996	A1 Div ex	US 6610472

PRIORITY APPLN. INFO: US 2000-703399 20001031; US 2003-423495 20030424; US 2004-947610 20040921

AN 2002-590677 [63] WPIDS

AB WO 200255718 A UPAB: 20021001
NOVELTY - A library of expression vectors encoding a library of protein complexes, comprising first and second nucleotide sequences (NS) which encode first or second polypeptide subunits (PS), respectively, is new.
DETAILED DESCRIPTION - A library of expression vectors encoding a library of protein complexes, comprising first and second nucleotide sequences (NS) which encode first or second polypeptide subunits (PS), respectively. The first and second NSs each independently vary within the library of expression vectors, and the first and second PSs are expressed

as separate proteins which self-assemble to form a protein complex in cells into which the library of expression vectors are introduced.

INDEPENDENT CLAIMS are also included for:

(1) a method for generating a library of yeast expression vectors;

(2) a method of producing a library of antibodies or antibody fragments;

(3) methods for selecting tester proteins or tester protein complexes capable of binding to a target peptide or protein; and

(4) a kit comprising a first and second populations of haploid yeast cells of opposite mating types, where:

(a) the first population of haploid yeast cells comprises a library of tester expression vectors for the library of tester fusion proteins, where each tester expression vector comprises:

(i) a first transcription sequence encoding either the activation domain or the DNA binding domain of the transcription activator;

(ii) a first nucleotide sequence encoding the first polypeptide subunit fused which is expressed as a fusion protein with either the activation domain or the DNA binding domain of the transcription activator; and

(iii) a second nucleotide sequence encoding the second polypeptide subunit which is expressed as a separate protein from the first polypeptide subunit; and

(b) the second population of haploid yeast cells comprises a target expression vector, where the target expression vector encodes:

(i) the activation domain or the DNA binding domain of the transcription activator which is not expressed by the library of tester expression vectors; and

(ii) a target sequence encoding the target protein or peptide, where either the first or second population of haploid yeast cells further comprises a reporter gene whose expression is under transcriptional control of the transcription activator.

USE - The expression vectors are useful in screening protein-protein or protein-DNA binding pairs, for screening of fully human antibody against a wide variety of targets, such as antigen or library of antigens associated with diseases, and for profiling functions of genes, particularly functional proteonomics, efficiently and economically. The selected proteins may be used in therapeutics and diagnosis of diseases including autoimmune diseases, cancer, transplant rejection, infectious diseases, and inflammation.

ADVANTAGE - An advantage of the process of generating, selecting and optimizing large, diverse libraries of antibodies mimics the process of natural antibody diversification and maturation in a mammal. The new method of producing libraries eliminates many requisite steps in the traditional construction of cDNA libraries, and provides efficient ways of screening for high affinity antibodies in eukaryotic cells in vivo.

Dwg.0/12

L3 ANSWER 10 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER: 2002-435324 [46] WPIDS

DOC. NO. CPI: C2002-123631

TITLE: Novel oligonucleotide linker or population of linkers for preparing polynucleotide libraries, comprises an oligonucleotide fixed portion and an oligonucleotide variable portion.

DERWENT CLASS: B04 D16

INVENTOR(S): HAYASHIZAKI, Y

PATENT ASSIGNEE(S): (RIKE) RIKEN KK; (HAYA-I) HAYASHIZAKI Y

COUNTRY COUNT: 23

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG

WO 2002028876 A2 20020411 (200246)* EN 96
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR
W: CA JP US
EP 1325118 A2 20030709 (200345) EN
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE TR
JP 2004510780 W 20040408 (200425) 148
US 2004166499 A1 20040826 (200457)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002028876	A2	WO 2001-JP8805	20011005
EP 1325118	A2	EP 2001-974719	20011005
		WO 2001-JP8805	20011005
JP 2004510780	W	WO 2001-JP8805	20011005
		JP 2002-532458	20011005
US 2004166499	A1	WO 2001-JP8805	20011005
		US 2003-398483	20031015

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1325118	A2 Based on	WO 2002028876
JP 2004510780	W Based on	WO 2002028876

PRIORITY APPLN. INFO: JP 2000-306749 20001005
AN 2002-435324 [46] WPIDS
AB WO 200228876 A UPAB: 20020722
NOVELTY - A linker (I) or a population of linkers comprising an oligonucleotide fixed portion and an oligonucleotide variable portion, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a double stranded linker or a population of linkers, comprising:

(a) a first oligonucleotide (ont1) single strand comprising an oligonucleotide single strand fixed portion and an oligonucleotide single strand variable portion; and

(b) a second oligonucleotide (ont2) single strand comprising an oligonucleotide single strand fixed portion annealed to he complementary oligonucleotide single strand fixed portion, so that the variable portion protrudes outside the double strand fixed portion of the linker;

(2) a population of linkers, comprising at least two (I);

(3) a linker-polynucleotide (II) or population of linker-polynucleotides comprising (I) or population of linkers and target first strand polynucleotide bound to the linker;

(4) a vector (II) comprising (II);

(5) preparing (I) or population of (I), by annealing ont1 to ont2, so that the variable portion protrudes outside the double strand fixed portion of the linker;

(6) binding a linker or population of linkers to mRNA, comprising treating mRNA with phosphatase and removing phosphate groups from uncapped mRNA, treating the product with pyrophosphatase, which removes the CAP structure from capped mRNA, and adding an RNA ligase in the presence of (I); and

(7) preparing a linker-polynucleotide, by treating mRNA by the method of (6), adding an RNA ligase in the presence of (I) or population of (I) and adding an oligo dT and synthesizing a polynucleotide complementary to the complete sequence of the mRNA.

USE - (I) is useful for binding a target single strand **polynucleotide** to a **linker**, by preparing (I) and

annealing the **variable** portion of first strand of (I) to the target single strand **polynucleotide** and ligating the fixed portion of the second strand of the **linker** to the target. The method is useful for preparing a second strand **polynucleotide**, by synthesizing the second strand complementary to the first. (I) is also useful for preparing a **linker-polynucleotide** comprising a **linker** and a double-strand **polynucleotide** , by annealing the **variable** portion of the **linker** to the target, and synthesizing the second strand. Ligation is performed by a ligase in the presence of a ligase-stimulating agent, preferably polyethylene glycol. The **linker** and the target is DNA. The single or double strand **polynucleotide** is a long strand, full coding and/or full-**length** cDNA. The first strand cDNA is obtained from the Cap trapping at the 5' end of the mRNA. The cap-trapping cDNA is further normalized or subtracted before or after the ligation to **linker**. The method comprises increasing temperature to 65 deg. C before annealing the **linker** to the target and/or after synthesizing the second strand. The **linker-polynucleotide** is cleaved at both ends in restriction enzyme sites and inserted into a vector. (I) facilitates the preparation of a DNA/RNA hybrid, which comprises providing a full-**length**/coding or long polyA mRNAs, ligating and annealing the mRNA to (I), where the **linker** comprises a restriction enzyme site, annealing an oligo dT-primer comprising second restriction enzyme site to the mRNA, synthesizing a cDNA strand, isolating the hybrid by using restriction enzymes which recognize two specific restriction enzyme sites introduced, and cloning. (I) is further useful for marking a **polynucleotide** library and distinguishing the library, where the fixed portion comprises a marker indicating a specific or defined tissue or species. (All claimed).

ADVANTAGE - The linkers facilitate the preparation of libraries more advantageously compared to conventional methods and in particular to the method of G-tailing. (I) does not require heavy metals and can be used at low temperature. The constant portion of (I) comprising a marker distinguishes and does not confuse libraries of different species.

Dwg.0/8

L3 ANSWER 11 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2002-090521 [12] WPIDS
DOC. NO. CPI: C2002-028001
TITLE: Screening libraries of tester proteins against protein, peptide or nucleic acid target(s) using a two-hybrid method in yeast, useful for generating recombinant human antibodies and screening for their affinity binding with target antigens.
DERWENT CLASS: B04 D16
INVENTOR(S): HUA, S B; ZHU, L
PATENT ASSIGNEE(S): (GENE-N) GENETASTIX CORP; (HUAS-I) HUA S B; (ZHUL-I) ZHU L
COUNTRY COUNT: 97
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2002000729	A2	20020103	(200212)*	EN	252
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
AU 2001071553	A	20020108	(200235)		

US 6406863 B1 20020618 (200244)
US 6410246 B1 20020625 (200246)
US 6410271 B1 20020625 (200246)
US 2003027213 A1 20030206 (200313)
EP 1297124 A2 20030402 (200325) EN
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR
US 2003165990 A1 20030904 (200359)
CN 1444651 A 20030924 (200382)
US 2005142562 A1 20050630 (200543)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002000729	A2	WO 2001-US20542	20010625
AU 2001071553	A	AU 2001-71553	20010625
US 6406863	B1	US 2000-603663	20000623
US 6410246	B1	US 2000-603658	20000623
US 6410271	B1	US 2000-602373	20000623
US 2003027213	A1 Div ex	US 2000-603663	20000623
		US 2002-112612	20020327
EP 1297124	A2	EP 2001-950579	20010625
		WO 2001-US20542	20010625
US 2003165990	A1 Div ex	US 2000-602373	20000623
		US 2002-112691	20020327
CN 1444651	A	CN 2001-813639	20010625
US 2005142562	A1 Div ex	US 2000-603663	20000623
	Cont of	US 2002-112612	20020327
		US 2004-792682	20040302

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2001071553	A Based on	WO 2002000729
US 2003027213	A1 Div ex	US 6406863
EP 1297124	A2 Based on	WO 2002000729
US 2003165990	A1 Div ex	US 6410271
US 2005142562	A1 Div ex	US 6406863

PRIORITY APPLN. INFO: US 2000-603663 20000623; US 2000-602373 20000623; US 2000-602972 20000623; US 2000-603658 20000623; US 2002-112612 20020327; US 2002-112691 20020327; US 2004-792682 20040302

AN 2002-090521 [12] WPIDS

AB WO 200200729 A UPAB: 20020221

NOVELTY - Methods for screening diverse libraries of tester proteins against protein, peptide or nucleic acid target(s) using a two-hybrid method in yeast, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are provided for the following:

(1) a method (M1) for selecting tester proteins capable of binding to a target peptide or protein, comprising:

(a) expressing a library of tester fusion proteins in yeast cells, each tester fusion protein comprising either an activation domain or a DNA binding domain of a transcription activator and a tester protein having a diversity of at least 1 x 107 within the library, the tester protein comprising a first polypeptide subunit whose sequence varies within the

library, a second polypeptide subunit whose sequence varies within the library independently of the first polypeptide, and a linker peptide which links the first and second polypeptide subunits;

(b) expressing a target fusion protein in the yeast cells expressing the tester fusion proteins, the target fusion protein comprising either the DNA binding domain or the activation domain of the transcription activator which is not comprised in the tester fusion proteins, and a target peptide or protein; and

(c) selecting those yeast cells in which a reporter gene is expressed, the expression of the reporter gene being activated by a reconstituted transcriptional activator formed by binding of the tester fusion protein to the target fusion protein;

(2) a kit, comprising:

(a) a first and second populations of haploid yeast cells of opposite mating types;

(b) a first population of haploid yeast cells comprising a library of tester expression vectors for the library of tester fusion proteins, each of the tester expression vector comprising a first transcription sequence encoding either an activation domain or a DNA binding domain of a transcription activator;

(c) a first nucleotide sequence encoding a first polypeptide subunit;

(d) a second nucleotide sequence encoding a second polypeptide subunit; and

(e) a linker sequence encoding a linker peptide that links the first nucleotide sequence and the second nucleotide sequence;

(f) a second population of haploid yeast cells comprises a target expression vector, the target expression vector encodes either the activation domain or the DNA binding domain of the transcription activator which is not expressed by the library of tester expression vectors; and

(g) a target sequence encoding the target protein or peptide; where either the first or second population of haploid yeast cells comprising a reporter construct comprises a reporter gene whose expression is under transcriptional control of the transcription activator;

(3) methods (M2) for generating a library of yeast expression vectors;

(4) a library of yeast expression vectors encoding a library of fusion proteins, each vector comprising:

(a) a first nucleotide sequence encoding a first polypeptide subunit;

(b) a second nucleotide sequence encoding a second polypeptide subunit; and

(c) a linker sequence encoding a linker peptide that links the first nucleotide sequence and the second nucleotide sequence, where the first polypeptide subunit, the second polypeptide subunit, and the linker polypeptide are expressed as a single fusion protein within the library of fusion proteins, and the first and second nucleotide sequences each independently varies within the library of expression vectors, and the diversity of the library of fusion proteins is at least 1 x 107; and

(5) kit, comprising a library of tester expression vectors and a yeast cell line, each of the tester expression vectors comprising:

(a) a first transcription sequence encoding either an activation domain or a DNA binding domain of a transcription activator;

(b) a first nucleotide sequence encoding a first polypeptide subunit;

(c) a second nucleotide sequence encoding a second polypeptide subunit; and

(d) a linker sequence encoding a linker peptide that links the first nucleotide sequence and the second nucleotide sequence, where the first and second nucleotide sequences each independently varies within the library of expression vectors.

USE - The method is useful for generating recombinant human antibodies and screening for their affinity binding with target antigens.

Dwg.0/21

L3 ANSWER 12 OF 23 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2001:247476 CAPLUS
DOCUMENT NUMBER: 134:276460
TITLE: Oligonucleotides of variable length and sequence for use as linker regions for dual-domain or multi-domain molecules
INVENTOR(S): Reinl, Stephen J.; Lindbo, John A.; Turpen, Thomas
PATENT ASSIGNEE(S): Large Scale Biology Corporation, USA
SOURCE: PCT Int. Appl., 77 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001023543	A1	20010405	WO 2000-US25965	20000922
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2385609	AA	20010405	CA 2000-2385609	20000922
EP 1218501	A1	20020703	EP 2000-965277	20000922
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL				
JP 2003510073	T2	20030318	JP 2001-526926	20000922
ZA 2002002066	A	20030313	ZA 2002-2066	20020313
PRIORITY APPLN. INFO.:			US 1999-155978P P	19990924
			WO 2000-US25965 W	20000922

AB Disclosed are methods and compns. for creating a DNA, RNA or protein mol. with two or more nucleic acid or polypeptide domains, resp., joined by a linker region. These methods are used to generate random linker libraries of nucleic acids that encode dual-domain or multi-domain polypeptides. The linker regions are characterized by both length and sequence variability but may be made of repeats of a triplet sequence. Rules for the generation of the triplets for use in the linkers are given. The linker oligonucleotides may also be selected to bind to a specific protein. The linkers can be incorporated into nucleic acids of interest by PCR and these can then be ligated via the linker domains. Methods for ligating these amplification products and the removal of artifacts such as hybridization bubbles are described. Use of these linkers to construct a gene for a single chain antibody and expression of the gene in transgenic tobacco are demonstrated.
REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 13 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2002-049243 [06] WPIDS
DOC. NO. CPI: C2002-013805
TITLE: New bispecific molecules, useful for targeting multiple epitopes of pathogenic antigen, comprise binding domains that bind to pathogenic antigenic molecule and C3b-like receptor, and does not contain antibody to CR1.
DERWENT CLASS: B04 D16
INVENTOR(S): HIMAWAN, J
PATENT ASSIGNEE(S): (ELUS-N) ELUSYS THERAPEUTICS INC; (HIMA-I) HIMAWAN J

COUNTRY COUNT: 96
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001080883	A1	20011101	(200206)*	EN	93
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
AU 2001057206	A	20011107	(200219)		
EP 1284752	A1	20030226	(200319)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR					
JP 2004506408	W	20040304	(200417)		140
US 2004180046	A1	20040916	(200461)		

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 2001080883	A1		WO 2001-US13161	20010424
AU 2001057206	A		AU 2001-57206	20010424
EP 1284752	A1		EP 2001-930698	20010424
			WO 2001-US13161	20010424
JP 2004506408	W		JP 2001-577980	20010424
			WO 2001-US13161	20010424
US 2004180046	A1	Provisional	US 2000-199903P	20000426
		Provisional	US 2000-244812P	20001101
			WO 2001-US13161	20010424
			US 2004-258650	20040303

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001057206	A	Based on	WO 2001080883
EP 1284752	A1	Based on	WO 2001080883
JP 2004506408	W	Based on	WO 2001080883

PRIORITY APPLN. INFO: US 2000-244812P 20001101; US 2000-199903P 20000426; US 2004-258650 20040303

AN 2002-049243 [06] WPIDS

AB WO 200180883 A UPAB: 20020128

NOVELTY - A bispecific molecule (I) comprising a first binding domain (B1) which binds to a pathogenic antigenic molecule (M1), a second binding domain (B2) which binds to a C3b-like receptor, and does not consist of a first monoclonal antibody to CR1 that has been chemically cross-linked to a second monoclonal antibody, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a nucleic acid (II) encoding (I);

(2) a cell (III) transformed with (II);

(3) a kit (K1) comprising (I) in a container, or one or more isolated nucleic acids encoding (I) in one or more containers;

(4) producing (I);

(5) a cell transformed with a first nucleotide sequence encoding B1 and a second nucleotide sequence encoding B2, where when expressed in the cell, B1 and B2 associate together to form (I);

(6) producing a bispecific immunoglobulin secreting cell, by fusing a first cell expressing an immunoglobulin that binds to a C3b-like receptor with a second cell expressing an immunoglobulin that binds to M1, and selecting for cells that express a bispecific immunoglobulin comprising B1 and B2;

(7) a bispecific antibody producing cell produced by the above method;

(8) a cell that secretes (I);

(9) a kit comprising in one or more containers, a first vector and a second vector, where the first vector comprises a first DNA sequence (S1) encoding at least a first immunoglobulin variable heavy chain domain fused through a polypeptide linker to a first immunoglobulin variable light chain domain, and the second vector comprises a second DNA sequence (S2) encoding at least a second immunoglobulin variable heavy chain domain fused through a polypeptide linker to a second immunoglobulin variable light chain domain, where the first immunoglobulin variable heavy chain domain and the first immunoglobulin variable light chain bind M1, and the second immunoglobulin variable heavy chain domain and second immunoglobulin variable light chain domain bind a C3b-like receptor;

(10) making a hematopoietic cell/(I) complex, by contacting (I) with hematopoietic cells that express a C3b-like receptor under conditions conducive to binding, such that a complex consisting essentially of a hematopoietic cell bound to one or more bispecific molecules is formed;

(11) a bispecific immunoglobulin comprising B1 and B2, produced by fusing a first cell expressing an immunoglobulin which binds to a C3b-like receptor with a second cell expressing an immunoglobulin which binds to M1, selecting for cells that express a bispecific immunoglobulin that binds to C3b-like receptor and binds to M1, culturing the selected cells, and recovering the bispecific immunoglobulin expressed by the cultured cells;

(12) a hematopoietic cell/(I) complex consisting essentially of a hematopoietic cell bound to one or more bispecific molecules;

(13) a polyclonal population (PP) of (I) comprising a number of bispecific molecules, each comprising different first antigen recognition region and a second antigen recognition region that binds a C3b-like receptor, where the different first antigen recognition regions having different binding specificities;

(14) a composition comprising a number of purified bispecific molecules, each comprising a first antigen recognition region that binds a C3b-like receptor and a second antigen recognition region that binds to M1, where each purified bispecific molecule comprises a different second antigen recognition portions that has a different binding specificity;

(15) a population (PN) of nucleic acids encoding PP;

(16) a population (PC) of cells transformed with PN;

(17) a kit comprising PN or PC in one or more containers;

(18) a pharmaceutical composition (C) comprising (I) or PP, effective to treat a mammal having an undesirable condition associated with the presence of M1; and

(19) producing PP.

ACTIVITY - Antiviral; antibacterial; antifungal; protozoacide; antiparasitic.

MECHANISM OF ACTION - Vaccine. No supporting data given.

USE - (I) is useful for preventing an undesirable condition associated with the presence of a pathogenic antigenic molecule in a mammal, by administering (I) prior to the onset of the undesirable conditions to the mammal. (I) is also useful for treating a mammal having an undesirable condition associated with the presence of a pathogenic antigenic molecule, by contacting (I) with hematopoietic cells expressing a C3b-like receptor, to form a hematopoietic cell/(I) complex. PP is useful for treating a mammal having an undesirable condition associated with the presence of a pathogenic antigenic molecule, by administering PP to the mammal. The pathogenic antigenic molecule is an antigen of a virus,

bacterium, fungus, protozoan or parasite (claimed). PP is also useful for targeting multiple epitopes and/or multiple variants of a pathogenic antigenic molecule. (C) is useful for rapidly and efficiently clearing antigens from circulation, and for the treatment of diseases, disorders and other conditions associated with antigens.

ADVANTAGE - (I) is suitable for rapid and efficient clearing of antigens from circulation.

DESCRIPTION OF DRAWING(S) - The figure shows the production of bispecific monoclonal antibodies.

1A, 1B, 1C/4

L3 ANSWER 14 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER: 2001-648443 [74] WPIDS

DOC. NO. CPI: C2001-191371

TITLE: Controlling cellular, organismal phenotypes comprises recombining conjoint polynucleotide segments to produce recombinant concatamer library which is expressed in cells and screened to identify cells with desired phenotype.

DERWENT CLASS: B04 C06 D16

INVENTOR(S): KEENAN, R J; MINSHULL, J; STEMMER, W P C

PATENT ASSIGNEE(S): (KEEN-I) KEENAN R J; (MINS-I) MINSHULL J; (STEM-I) STEMMER W P C; (MAXY-N) MAXYGEN INC

COUNTRY COUNT: 95

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001073000	A2	20011004	(200174)*	EN	93
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
US 2001049104	A1	20011206	(200203)		
AU 2001087273	A	20011008	(200208)		
EP 1276861	A2	20030122	(200308)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR					
US 2004203046	A1	20041014	(200468)		

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 2001073000	A2		WO 2001-US9203	20010323
US 2001049104	A1	Provisional	US 2000-191782P	20000324
		Provisional	US 2001-262617P	20010117
			US 2001-817015	20010323
AU 2001087273	A		AU 2001-87273	20010323
EP 1276861	A2		EP 2001-962421	20010323
			WO 2001-US9203	20010323
US 2004203046	A1	Provisional	US 2000-191782P	20000324
		Provisional	US 2001-262617P	20010117
		Cont of	US 2001-817015	20010323
			US 2004-832780	20040427

FILING DETAILS:

PATENT NO	KIND	PATENT NO

AU 2001087273 A Based on WO 2001073000
EP 1276861 A2 Based on WO 2001073000

PRIORITY APPLN. INFO: US 2001-262617P 20010117; US
2000-191782P 20000324; US
2001-817015 20010323; US
2004-832780 20040427

AN 2001-648443 [74] WPIDS

AB WO 200173000 A UPAB: 20011217

NOVELTY - Controlling, (I), a phenotype comprising recombining or mutating a population of conjoint polynucleotide (PN) segments (CPS) comprise, encode or modulate a phenotype, to produce a library, introducing the library into a population of recipient cells or intracellular organelles and identifying a cell, organelle, or organism comprising a cell with a desired phenotype, is new.

DETAILED DESCRIPTION - Controlling (I) a phenotype comprises recombining or mutating a population of conjoint polynucleotide (PN) segments (CPS) where one or more CPS comprise, encode or modulate a phenotype, to produce a library of recombinant concatamers, introducing the library into a population of recipient cells or intracellular organelles and identifying a cell, organelle, or organism comprising a cell with a desired phenotype.

INDEPENDENT CLAIMS are also included for the following:

(1) modulating (II) activity of one or more targets, by providing a library of PN segments encoding several peptides, which are pre-selected for one or more desired properties which are same or different between peptides, joining the pre-selected PN segments to generate a population of CPS which are operably linked to at least one transcription regulatory sequence, expressing one or more of CPS in vitro or in vivo which produces one or more multipeptides comprising several peptide segments which are optionally joined by a linker sequence and identifying one or more CPS encoding a multipeptide comprising a peptide capable of modulating activity of one or more targets;

(2) producing (III) a library of preselected peptides by providing a library of nucleic acids encoding fusion polypeptides which are capable of displaying one or more variable peptide moieties in vitro or in vivo, expressing the fusion polypeptides such that the one or more variable peptide moieties are displayed in vitro or in vivo and identifying several variable peptide moieties with a desired property which produces a library of pre-selected peptides;

(3) a library of pre-selected peptide produced by the above method;

(4) a library (IV) of nucleic acids comprising several CPS which alter expression of one or more components of an endogenous phenotype, operably linked to a transcription regulatory sequence;

(5) a library comprising population of CPS;

(6) a recombinant episomal vector contained in CPS; and

(7) a cell or an organism comprising a cell produced by (I).

USE - (I) is useful for controlling a phenotype including oil content or composition, fat content or composition, sugar content or composition, starch content or composition, protein content or composition, phytochemical content or composition, nutraceutical content or composition, yield, time to maturity, growth rate, height at maturity, carbon-fixation rate, tolerance to salt, heat, cold, drought, water, heavy metal, radiation, resistance to a chemical composition, disease resistance, insect, parasite resistance, color, fluorescence, height, weight, density, toxicity, flavor, sweetness, bitterness, nutritional activity or therapeutic activity. The phenotype is regulated by at least one epigenetic mechanism such as chromatin silencing, methylation, maternal effects, regulation by cytoplasmic factors, antisense suppression, sense suppression, cosuppression, promoter alteration, DNA recombination, homology-dependent mechanisms, aminoacylation and post-transcriptional gene silencing comprising silencing by a dominant

negative inhibitor, a transdominant inhibitor or a peptide inhibitor. (II) is useful for modulating activity of one or more targets comprising a class of enzymes such as proteases, lipases, esterases, hydrolases or amylases, intracellular, extracellular and cell-surface molecules. (III) is useful for producing a library of pre-selected peptides comprising in excess of 100-1000000 different members (all claimed). The multigenic phenotypes modulated include cell cycle state, cell cycle progression, cell morphology, DNA replication activity, transcriptional activity, nucleic acid recombination activity, meiosis, timing and quantity of secondary metabolite production.

ADVANTAGE - The method provides simple and rapid processes for screening and optimizing peptides that modulate the activity of cellular targets such as enzymes.

DESCRIPTION OF DRAWING(S) - The figure shows the schematic illustration showing the correspondence of multiple genetic elements that make up an episomal vector comprising conjoint polynucleotide segments with multiple genes of a genetic or metabolic pathway.

Dwg.1/6

L3 ANSWER 15 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER: 2001-596845 [67] WPIDS

DOC. NO. CPI: C2001-176623

TITLE: Novel probe sets with common universal linkers at one or both ends (WRAP probes) for gene expression arrays to provide global amplification of probe set and to provide common equivalent signaling regardless of length.

DERWENT CLASS: B04 D16

INVENTOR(S): SHAFER, D A

PATENT ASSIGNEE(S): (GENE-N) GENETAG TECHNOLOGY INC; (SHAF-I) SHAFER D A

COUNTRY COUNT: 95

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001066802	A1	20010913	(200167)*	EN	97
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
AU 2001043523	A	20010917	(200204)		
US 2004053275	A1	20040318	(200421)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001066802	A1	WO 2001-US7508	20010309
AU 2001043523	A	AU 2001-43523	20010309
US 2004053275	A1	WO 2001-US7508	20010309
		US 2003-380596	20030317

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001043523	A	Based on	WO 2001066802

PRIORITY APPLN. INFO: US 2000-187982P 20000309; US 2003-380596 20030317

AN 2001-596845 [67] WPIDS

AB WO 200166802 A UPAB: 20011119

NOVELTY - Probe set (I) for gene expression arrays to provide common equivalent signaling per probe and global amplification of (I), having pool of modified cDNA probes (II) copied from sample of mRNA transcripts, where each single stranded (II) has universal linker (UL) located on its terminal end, is new.

DETAILED DESCRIPTION - Each single stranded (I) comprises a central target specific segment copied from a portion of a single mRNA transcript and a universal linker (UL) located on a terminal end of the probe. (UL) comprises reporter binding sites to join common reporters to the probes and primer binding sites to copy and amplify the probe.

INDEPENDENT CLAIMS are also included for the following:

(1) an (UL) composition (III), suitable for gene expression arrays and related hybridization assays having multiple nucleic acid target sequences affixed in known locations to a substrate, comprises a nucleotide linking sequence (LS) which can be globally appended to a terminal end of each probe in an initial probe set derived from mRNA transcripts of an analyte sample to produce a final set of probes where the appended (LS) is not complementary to the target sequences of the assay. The appended (LS) can serve as a universal primer binding site for copying and amplifying the final probe set and is suitable for binding to a complementary nucleotide linking sequence of a reporter or a multi-linker;

(2) a set (IV) of two or more (III), where (III) in the set comprise nucleotide (LS) which can bind two or more sets of probes to two or more different common reporters;

(3) a modified poly-T primer composition (V) to initiate reverse transcriptase (RT) and to convert mRNA transcripts into (I) with one or more (UL) attached to each probe, comprises a polynucleotide (PN) unit having a poly-T sequence on the 3' end and (UL) sequence on the 5' end, where the poly-T sequence comprises a series of thymidine bases in the range of about 12-20 thymidines;

(4) a specific adapter composition (VI) to append (UL) to 3' ends of the probes of (I), comprises two PNs joined together by hybridized complementary bases which comprise a set of (UL) sequences and one of the PNs further comprises a short overhang of single stranded bases that specifically match and bind to terminal sequences of a probe cut with a specific restriction enzyme. The short overhang comprises a set of specific bases matching a restriction cut site, where the set of specific bases is in the range of 2-8 specific bases;

(5) a random adapter composition (VII) to append (UL) to 3' ends of the probes of a (I), comprises two PNs joined as in (VI) above, where the short overhang comprises a series of randomly synthesized variable bases of adenine, cytosine, guanine, or thymidine in the range of 1-6 randomly variable bases;

(6) a homopolymeric adapter composition (VIII) to append (UL) to 3' ends of the probes of a (I), comprises two PNs joined as in (VII) above, where the short overhang comprises a series of solely cytosine bases or solely guanine bases on the range of about 6-18 bases;

(7) a random extender composition (IX) to randomly bind to a probe and provide terminal template, comprises a single-stranded PN having a 5' end and a 3' end, where the 5' end comprises (UL) and the 3' end comprises a random sequence, where the random sequence comprises randomly synthesized variable bases of adenine, cytosine, guanine, or thymidine in a range of about 4-10 randomly variable bases;

(8) a homopolymeric extender composition (X) to bind to a 3' end of a probe tailed with Poly-G or Poly-C sequences using terminal transferase, comprises a single-stranded PN having a 3' end and a 5' end where the 5' end comprises at least one (UL) and the 3' end comprises a poly-C or poly-G homopolymeric sequence and the homopolymeric sequence comprises a series, respectively, of solely cytosine bases or solely guanine bases in the range of about 5-15 bases;

(9) an (UL)-primer-reporter composition (XI), comprises a PN with label and (UL), where (UL) comprises a primer sequence;

(10) a set of probe modifiers (XII) to allow comparisons of different probe sets, comprising several subsets of a type such as (V)-(XI), where each subset employed with a probe set comprises a different (UL) sequence;

(11) making (M1) (WRAP probe method) and applying (I) for gene expression analysis which provides more accurate quantitative detection by attaching common reporters to terminal linkers of the probes in the probe set, involves providing RNA from a tissue sample; making (II) from the RNA transcripts with universal linkers at one or both ends; hybridizing (II) to an array or series of gene specific targets; joining reporters to (II); and detecting reporters to determine expression of genes in the tissue sample;

(12) a gene expression array analysis method (M2) (mini WRAP probe method), particularly for oligonucleotide-based arrays, to make multiple double-linker probes from each transcript of a RNA sample, suitable for exponential amplification and labeling, by attaching (UL)s to the terminal ends of a probe set comprising fragmented (II); and

(13) determining (M3) full length cDNA sequences at the 5' end of a mRNA transcript, where (IX) is employed to find and duplicate the absolute 3' end of first strand cDNA copies of a specific gene, comprises:

(a) providing a set of mRNA transcripts where the 5' end of the gene of interest has been copied as first strand antisense cDNA by reverse transcriptase using a gene specific primer that comprises a (UL) and a capture moiety;

(b) capturing and purifying the first strand cDNA copies of the targeted transcripts;

(c) applying (IX) with rapid thermal cycling to extend the 3' end of the cDNA product with a (UL) sequence, where a double-linker product is formed suitable for PCR amplification; and

(d) amplifying and sequencing the double-linker cDNA product to determine the sequences of the 5' end of the gene.

USE - The probes and reporters are useful in diagnostic or drug discovery assays for a wide range of biomedical samples, including detection of nucleic acids and gene expression profiles in human diagnostics, forensics and genomic analysis (disclosed).

(M2) is useful for amplifying and identifying any unknown DNA fragment or set of fragments. In addition, (M2) may be used for improving sensitivity with tissue microarrays or RNA arrays, where cDNA probe fragments are modified by appending (UL)s to one or both ends of the probe (claimed).

ADVANTAGE - The probe set provides common equivalent signaling per probe regardless of length and provides global amplification. Methods using (I) improve the quantification of gene expression and allow highly improved detection of rare transcripts and/or very small samples.

Dwg.0/11

L3 ANSWER 16 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER: 2001-536643 [59] WPIDS

CROSS REFERENCE: 2004-121559 [12]

DOC. NO. CPI: C2001-159819

TITLE: Detecting abnormal base-pairing, mutation in nucleic acid, or polymorphism in gene locus, comprises contacting nucleic acid with abnormal base-pairing and mutant nucleic acid repair enzyme, and detecting their binding.

DERWENT CLASS: B04 D16

INVENTOR(S): YUAN, C

PATENT ASSIGNEE(S): (GEAT) GEN ATOMICS

COUNTRY COUNT: 93

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG

WO 2001062968 A2 20010830 (200159)* EN 294
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW
AU 2001027679 A 20010903 (200202)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001062968	A2	WO 2001-US452	20010105
AU 2001027679	A	AU 2001-27679	20010105

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001027679	A	Based on	WO 2001062968

PRIORITY APPLN. INFO: US 2000-514016 20000225
AN 2001-536643 [59] WPIDS
CR 2004-121559 [12]
AB WO 200162968 A UPAB: 20040218

NOVELTY - Detecting (M1) abnormal base-pairing in a nucleic acid duplex, mutation in a nucleic acid or polymorphism in a gene locus, comprising contacting a nucleic acid duplex having an abnormal base-pairing with a mutant nucleic acid repair enzyme (I) or its complex, and detecting the binding between the nucleic acid duplex and (I), such that the presence of abnormal base-pairing, mutation or polymorphism is detected, is new.

DETAILED DESCRIPTION - M1 comprises:

(a) detecting abnormal base-pairing in a nucleic acid duplex, by contacting a nucleic acid duplex having or suspected of having a abnormal base-pairing with (I), where (I) has binding affinity for the abnormal base-pairing in the duplex but has attenuated catalytic activity compared to the wild-type enzyme, and detecting the binding between the nucleic acid duplex and (I), where the presence or quantity of the abnormal base-pairing in the duplex is assessed;

(b) detecting a mutation in a nucleic acid, by hybridizing a strand of a nucleic acid having or suspected of having a mutation with a complementary strand of a nucleic acid fragment having a wild type sequence, such that the mutation results in an abnormal base-pairing in the formed nucleic acid duplex, contacting the nucleic acid duplex with (I), and detecting binding between the nucleic acid duplex and (I), such that the presence or quantity of the mutation is assessed; or

(c) detecting polymorphism in a gene locus, by hybridizing a target strand of a nucleic acid comprising a locus to e tested with a complementary reference strand of a nucleic acid comprising a known allele of the locus, such that the allelic identity between the target and the reference strands results in the formation of a nucleic acid duplex without an abnormal base-pairing and the allelic difference between the target and the reference strands results in the formation of a nucleic acid duplex with an abnormal base-pairing, contacting the nucleic acid duplex with (I), and detecting binding between the nucleic acid duplex and (I), such that the polymorphism in the locus is assessed.

INDEPENDENT CLAIMS are also included for the following:

(1) purifying or separating (M2) nucleic acid duplex containing one or more abnormal base-pairing from a population of nucleic acid duplexes, by contacting a population of nucleic acid duplexes having or suspected of

having a nucleic acid duplex containing one or more abnormal base-pairing with (I), where the nucleic acid duplex containing one or more abnormal base-pairing binds to (I) to form a binding complex, and removing the nucleic acid duplexes that contain the binding complex from the population of nucleic acid duplexes;

(2) detecting and localizing (M3) an abnormal base-pairing in a nucleic acid duplex, by contacting a nucleic acid duplex having or suspected of having an abnormal base-pairing with (I) to form a binding complex, subjecting the nucleic acid duplex to hydrolysis with an exonuclease under conditions such that the binding complex blocks hydrolysis, and determining the location within the nucleic acid duplex protected from the hydrolysis, and thus detecting and localizing the abnormal base-pairing in the nucleic acid duplex;

(3) a combination (C1) for detecting abnormal base-pairing in a nucleic acid duplex, comprising (I), and a reagent for detecting binding between abnormal base-pairing in a nucleic acid duplex and (I);

(4) a kit comprising C1 and instructions for binding (I) to nucleic acid duplexes to detect a mutation in a nucleic acid duplex, to detect a polymorphism in a locus, to diagnose diseases or disorders, or for gene mapping or identification by detecting a number of polymorphisms or mutations;

(5) an isolated substantially pure (I) comprising a detectable label, and having attenuated catalytic activity compared to the wild-type but retaining binding affinity for a nucleic acid duplex containing an abnormal base-pairing;

(6) an article of manufacture, comprising a packaging material, (I), and a label indicating that the article is for use in detecting abnormal base-pairing in a nucleic acid duplex;

(7) a combination (C2) for detecting and localizing an abnormal base-pairing in a nucleic acid duplex, comprising (I) and an exonuclease; and

(8) a kit comprising C2 and instructions for performing an assay for detecting and localizing an abnormal base-pairing a nucleic acid duplex.

USE - The method is useful for prognosis or diagnosis of the presence or severity of the disease, disorder or infection by a pathological agent, associated with the mutation, including cancer, immune system disorder, metabolism disorder, muscle and bone disorder, nervous system disorder, signal disorder and transporter disease or disorder (claimed).

ADVANTAGE - The method is rapid and accurate, and is amenable to high throughput formats. The method requires neither specific probes nor gel electrophoresis. The method is amendable to automation for simultaneous detection of a large number of nucleic acid mutations.

Dwg.0/0

L3 ANSWER 17 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2001-451857 [48] WPIDS
CROSS REFERENCE: 2001-032034 [04]; 2004-203222 [19]
DOC. NO. NON-CPI: N2001-334488
DOC. NO. CPI: C2001-136526
TITLE: Interaction-dependent enzyme association systems for detecting interactions between two or three polypeptides, especially in human therapeutics, diagnostics or prognostics, comprise circularly permutated proteins.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): BALINT, R F; HER, J
PATENT ASSIGNEE(S): (PANO-N) PANORAMA RES INC; (KALO-N) KALOBIOS INC; (BALI-I) BALINT R F; (HERJ-I) HER J
COUNTRY COUNT: 95
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG

WO 2001051629 A2 20010719 (200148)* EN 104
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW
AU 2001036475 A 20010724 (200166)
EP 1248840 A2 20021016 (200276) EN
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR
US 2003165825 A1 20030904 (200359)

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 2001051629	A2		WO 2001-US1651	20010116
AU 2001036475	A		AU 2001-36475	20010116
EP 1248840	A2		EP 2001-908627	20010116
			WO 2001-US1651	20010116
US 2003165825	A1	Provisional	US 2000-175968P	20000113
		CIP of	US 2000-526106	20000315
			US 2001-764163	20010116

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001036475	A	Based on	WO 2001051629
EP 1248840	A2	Based on	WO 2001051629

PRIORITY APPLN. INFO: US 2000-526106 20000315; US 2000-175968P 20000113; US 2001-764163 20010116

AN 2001-451857 [48] WPIDS

CR 2001-032034 [04]; 2004-203222 [19]

AB WO 200151629 A UPAB: 20040318

NOVELTY - New interaction-dependent enzyme association (IdEA) systems comprise a fusion sequence that encodes for a circularly permutated, interaction-activated proteins that reassemble to form functionally reconstituted marker proteins which produce a detectable signal upon the association of two oligopeptides, or upon simultaneous association of two oligopeptides with a third oligopeptide.

DETAILED DESCRIPTION - New interaction-dependent enzyme association (IdEA) systems comprise a nucleic acid sequence encoding a first oligopeptide and a second oligopeptide, each fused in frame through a first and a second break-point terminus, respectively, to a circularly permutated marker protein. The circularly permutated marker protein reassembles to form a functionally reconstituted marker protein that produces a detectable signal upon the association of the first oligopeptide with the second oligopeptide, or upon simultaneous association of the first oligopeptide and the second oligopeptide with a third oligopeptide.

INDEPENDENT CLAIMS are also included for the following:

(1) identifying:

(a) a second oligopeptide to which a first oligopeptide binds; or

(b) a third oligopeptide to which a first oligopeptide and a second oligopeptide simultaneously bind; where method comprises employing the IdEA systems;

(2) an intracellular signal transduction biosensor comprising a first nucleic acid sequence encoding a first intracellular polypeptide and a

second intracellular polypeptide, each fused in frame through a first and a second break-point terminus, respectively, to a circularly permutated beta -lactamase, where the circularly permutated beta -lactamase reassembles to form a functionally reconstituted marker protein that produces a detectable signal upon the association of the first oligopeptide with the second oligopeptide or upon simultaneous association of the first oligopeptide and the second oligopeptide with the third intracellular polypeptide encoded by the second nucleic acid sequence;

(3) an expression cassette comprising, as operably linked components in the direction of transcription, nucleotide sequences encoding for:

(i) a promoter functional in a host cell;

(ii) a first polypeptide interactor domain;

(iii) a circularly permutated marker protein; or

(iv) a second polypeptide interactor domain;

(4) plasmids comprising the expression cassette;

(5) host cells comprising the plasmid;

(6) a DNA sequence comprising, as operably linked components in the direction of transcription, nucleic acid sequences encoding a first interactor domain, a circularly permutated marker protein or a second interactor domain, where the circularly permutated marker protein functionally reassembles upon binding of the first and the second interactor domains to each other or simultaneously to a third polypeptide;

(7) a circularly permutated marker protein fused in frame through each of its N- and C- termini to a first interactor domain and a second interactor domain, where the circularly permutated marker protein functionally reassembles upon the binding of the first and the second interactor domains to each other or simultaneously to a third polypeptide; and

(8) high-throughput identification of compounds that inhibit phosphorylation-regulated cell signal transducers comprising expressing from a plasmid in a host cell the oligopeptide having in the direction of translation, a first interactor domain, a circularly permutated beta -lactamase, and a second interactor domain, where the first interactor domain comprises a phosphorylation regulated cell signal transducer protein and the second interactor domain only under the required state of phosphorylation, where the first interactor domain with the second interactor domain results in the functional reconstitution of the circularly permutated beta -lactamase to produce a colored host cell in the presence of chromogenic beta -lactamase substrate and production of a colored host cell is indicative of a compound that inhibits phosphorylation-regulated cell signal transduction.

USE - The IdEA systems are useful for detecting and identifying interactions between intracellular as well as extracellular proteins, particularly between two or three polypeptides. The systems are also useful in selecting with a single marker protein the incorporation of multiple genetic traits in a host cell. In particular, the systems are useful in many applications in human therapeutics, diagnostics and prognostics, as well as in high-throughput screening systems for the discovery and validation of pharmaceutical targets and drugs.

ADVANTAGE - Prior systems (e.g. E. coli Dimer Detection System, yeast two-hybrid system or Selective Infective Phage System) require multiple steps between interaction and phenotype, which cause severe loss of efficiency due to high false positive and false negative rates. The present system is capable of simultaneous detection of multiple interactions between extra-cellular as well as intracellular proteins in a high throughput format.

Dwg.0/12

L3 ANSWER 18 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2001-450361 [48] WPIDS
CROSS REFERENCE: 2000-206023 [18]
DOC. NO. CPI: C2001-135958

TITLE: Analyzing a polynucleotide produced by amplifying cDNA or genomic DNA involves hybridizing terminus probes having constant and variable region to adapter-modified restriction fragment generated from the polynucleotide.
DERWENT CLASS: B04 D16
INVENTOR(S): HUNKAPILLER, M W; RICHARDS, J H
PATENT ASSIGNEE(S): (PEKE) PERKIN-ELMER CORP
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 6258539	B1	20010710	(200148)*		19

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 6258539	B1 CIP of	US 1998-135381	19980817
		US 1999-303774	19990430

PRIORITY APPLN. INFO: US 1999-303774 19990430; US 1998-135381 19980817
AN 2001-450361 [48] WPIDS
CR 2000-206023 [18]
AB US 6258539 B UPAB: 20010829
NOVELTY - Analyzing a polynucleotide by forming restriction fragment (RF) having first, second terminus and a termini generated by restriction endonuclease (RE), from the polynucleotide, joining an adapter to a terminus of RF to produce adapter-modified RF (I) and hybridizing a terminus probe having constant and variable region to single strand of (I) at a position including the terminus generated by RE.

USE - Analyzing a polynucleotide which is a cDNA or genomic DNA, or which is produced by amplifying a portion of a cDNA preparation or a portion of genomic DNA preparation (claimed).

The method allows simultaneous analysis of multiple different polynucleotides of polynucleotide composition e.g., cDNA or genomic DNA libraries, and the isolation of polynucleotides of interest identified through the analytical techniques. The analysis of RNA populations has utilities in research, diagnosis or treatment of a variety of diseases. The base sequence information contained within identifier sequences can be used to detect, discover or compare polymorphic sequences, to develop oligonucleotide primers to isolate the polynucleotide from which a specific identifier sequence is derived.

Analysis of large complex populations of polynucleotides may be used to produce sufficient information about a polynucleotide population so that differences between polynucleotide populations may be ascertained. Thus fingerprints of a polynucleotide population may be compared with fingerprints of other complex polynucleotide populations.

ADVANTAGE - The method permits the simultaneous analysis of a large number of different mRNA molecules that form a given mRNA population. Multiple identifier sequences may be obtained in parallel, thus permitting the rapid characterization of the large number of polynucleotides.

DESCRIPTION OF DRAWING(S) - The figure shows the terminus probes which hybridize to adapter-modified representative restriction fragments.
Dwg.1A/7

L3 ANSWER 19 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2001-032034 [04] WPIDS
CROSS REFERENCE: 2001-451857 [48]; 2004-203222 [19]
DOC. NO. NON-CPI: N2001-025000

DOC. NO. CPI: C2001-009858
TITLE: Novel fragment complementation system to identify interactions between polypeptides comprises fragment pairs having first and second members that reassemble into a marker protein which has a directly detectable signal.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): BALINT, R F; HER, J
PATENT ASSIGNEE(S): (PANO-N) PANORAMA RES INC
COUNTRY COUNT: 91
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000071702	A1	20001130	(200104)*	EN	94
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ TZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW					
AU 2000060459	A	20001212	(200115)		
EP 1183347	A1	20020306	(200224)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					
JP 2003500051	W	20030107	(200314)		116

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000071702	A1	WO 2000-US7108	20000316
AU 2000060459	A	AU 2000-60459	20000316
EP 1183347	A1	EP 2000-946748	20000316
		WO 2000-US7108	20000316
JP 2003500051	W	JP 2000-620079	20000316
		WO 2000-US7108	20000316

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2000060459	A	Based on	WO 2000071702
EP 1183347	A1	Based on	WO 2000071702
JP 2003500051	W	Based on	WO 2000071702

PRIORITY APPLN. INFO: US 2000-175968P 20000113; US 1999-135926P 19990525
AN 2001-032034 [04] WPIDS
CR 2001-451857 [48]; 2004-203222 [19]
AB WO 200071702 A UPAB: 20040318
NOVELTY - A fragment complementation system (I) which comprises a first oligopeptide (OP1) containing an N-terminal fragment with a C-terminal break point and a second oligopeptide (OP2) comprising a C-terminal with a N-terminal breakpoint, in which the C and N terminal fragments are both derived from a marker protein (MP) and reassemble to form a functionally reconstituted MP, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) identifying (M1) a functional fragment pair (FP) in a protein by preparing fragments of MP to obtain a marker fragment library (II), expressing members of (II) in many host cells, isolating host cells

expressing MP as indicative of a cell containing first and second member of a FP which have formed a functionally reconstituted MP, by which the functional FP is identified. Each fragment of MP prepared has a break point terminus within a solvent exposed group of MP, in which the N or C terminal residue of each C or N terminal fragment, respectively constitutes the break point terminus to obtain (II);

(2) an expression cassette (III) comprising as operably linked components in the direction of transcription, nucleotide sequences encoding for:

(i) a promoter functional in a host cell, a polypeptide interactor domain, FPL and C-terminal fragment of MP that provides for a selectable phenotype; or

(ii) a promoter functional in a host cell, an N-terminal fragment of a protein that provides for a selectable phenotype, FPL and a polypeptide interactor domain);

(3) identifying a OP2 to which a OP1 binds by:

(i) co-expressing in several host cells, OP1 and OP2 (which is a encoded by a member of a library) as a fusion protein with first and second members of FP of an MP, respectively, in which the binding of the OP1 to the OP2 results in functional reassembly of MP;

(ii) isolating host cells expressing the MP as indicative of a cell containing OP1 and OP2 which have interacted; and

(iii) sequencing plasmids containing expression cassettes coding for the fusion proteins, by which the OP2 to which the OP1 binds is identified; and

(4) host cells comprising expression cassettes (i) and (ii) of (2).

USE - The methods are used for monitoring the occurrence of protein-protein interactions in a sample, identifying oligopeptide interactions between two different proteomes, identifying epitopes that bind to an immunoglobulin (Ig) variable region, for identifying interactions between an extracellular domain of a transmembrane protein and a polypeptide, for high-throughput identification of compounds that inhibit phosphorylation-regulated signal transducers, forming a enzyme complementation system for selecting simultaneous incorporation of multiple genetic elements into a host cell and for activating a beta -lactam derivative of an antitumor compound in a host who is in need of it (all claimed).

(I) is used in human therapeutics, diagnostics and prognostics as well as in high-throughput systems for the discovery and validation of pharmaceutical targets and drugs. The interaction-activated enzyme association systems comprising prokaryotic beta -lactamase, are useful for simple and multiplex protein-protein interaction mapping, to enrich randomly primed expressed sequenced libraries for fragments which encode autonomously folding domains. It is also useful for interface mapping and ligand identification by mimotope homology, as bio-action sensors, in homogeneous assays and in target activated enzyme prodrug therapy (TAcEPT) and target-activate enzyme imaging (TAcEI). FP that comprise molecular interaction-dependent enzymes find use in homogeneous assays and biosensors for any analyte having two or more independent binding sites, tissue-localized activation of therapeutic and imaging reagents in vivo for early detection and treatment of cancer, chronic inflammation, atherosclerosis, amyloidosis, infection, transplant rejection, and other pathologies, cell-based sensors for activation or inhibition of metabolic or signal transduction pathways for high-efficiency, high-throughout screening for agonists/antagonists of the target pathway, high-throughput mapping of pair-wise protein-protein interactions within and between the proteomes of cell, tissues, and pathogenic organisms, rapid selection of antibody fragments or other binding proteins which bind specifically to polypeptides of interest, rapid antigen identification for anti-cell and anti-tissue antibodies, rapid epitope identification for antibodies and in cell-based screens for high-throughput selection of inhibitors of any protein-protein interaction.

ADVANTAGE - Inclusion of a reporter protein in (I) provides for a directly detectable signal upon reassembly and background levels of 1 in 106. The system further provides for rationally incorporated enhancement modifications to the fusion oligopeptides that increase the functional activity of the reconstituted protein to wild type levels by improving folding and reassembly of the fragments into the parent protein while at the same time maintaining dependence on the interactor domains for reassembly.

DESCRIPTION OF DRAWING(S) - The figure shows a mechanism for interaction-dependent enzyme activation.

Dwg.1/11

L3 ANSWER 20 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER: 2000-611449 [58] WPIDS

CROSS REFERENCE: 1999-287950 [24]; 2001-557931 [62]

DOC. NO. CPI: C2000-182935

TITLE: Making immobilized nucleic acid molecule array comprises creating array nucleic acid capture activity spots to which an excess of nucleic acid molecules with excluded volume greater than spots are contacted.

DERWENT CLASS: A89 B04 D16

INVENTOR(S): CHURCH, G M; MITRA, R D; MITRA, R

PATENT ASSIGNEE(S): (HARD) HARVARD COLLEGE

COUNTRY COUNT: 23

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000053812	A2	20000914	(200058)*	EN	117
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE					
W: AU CA JP					
AU 2000038761	A	20000928	(200067)		
EP 1235929	A2	20020904	(200266)	EN	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					
US 6485944	B1	20021126	(200281)		
EP 1291354	A2	20030312	(200320)	EN	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					
CA 2411514	A1	20000914	(200329)	EN	
JP 2003526331	W	20030909	(200360)		135
AU 2002301870	A1	20030313	(200433)#		
AU 2005201991	A1	20050602	(200541)#		

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 2000053812	A2		WO 2000-US6390	20000310
AU 2000038761	A		AU 2000-38761	20000310
EP 1235929	A2		EP 2000-917853	20000310
			WO 2000-US6390	20000310
US 6485944	B1	Provisional	US 1997-61511P	19971010
		Provisional	US 1998-76570P	19980302
		CIP of	US 1998-143014	19980828
			US 1999-267496	19990312
EP 1291354	A2	Div ex	EP 2000-917853	20000310
			EP 2002-79758	20000310
CA 2411514	A1	Div ex	CA 2000-2370535	20000310
			CA 2000-2411514	20000310
JP 2003526331	W		JP 2000-603433	20000310
			WO 2000-US6390	20000310
AU 2002301870	A1	Div ex	AU 2000-38761	20000310
			AU 2002-301870	20021107

AU 2005201991	A1 Div ex	AU 2000-38761	20000310
		AU 2005-201991	20050511

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2000038761	A Based on	WO 2000053812
EP 1235929	A2 Based on	WO 2000053812
EP 1291354	A2 Div ex	EP 1235929
JP 2003526331	W Based on	WO 2000053812

PRIORITY APPLN. INFO: US 1999-267496 19990312; US
1997-61511P 19971010; US
1998-76570P 19980302; US
1998-143014 19980828; AU
2002-301870 20021107; AU
2005-201991 20050511

AN 2000-611449 [58] WPIDS
CR 1999-287950 [24]; 2001-557931 [62]
AB WO 200053812 A UPAB: 20050629

NOVELTY - Making (M1) immobilized nucleic acid molecule array (N) comprises creating array of spots of nucleic acid capture activity (I) contacting (I) with excess of (N) with an excluded column diameter greater than the diameter of the spots of (I), resulting in (N), in which each spot of (I) can bind only (N) with excluded volume diameter greater than size of spots of (I).

DETAILED DESCRIPTION - The spots of the capture activity are separated by a distance greater than diameter of the spots and size of the spots is less than the diameter of the excluded volume of nucleic acid molecule to be captured.

INDEPENDENT CLAIMS are also included for the following:

(1) detecting (M2) a nucleic acid on (N) comprising generating multiple (N) in which the nucleic acid molecules of each unit of (N) occupy positions which corresponds to those positions occupied by the nucleic acid molecules of each unit of the multiple (N) array and then subjecting one or more units of the multiple (N) (but at least one less than the total number of the multiple (N)) to a method of signal detection which involves a signal amplification method that renders each member of the multiple nucleic acid array non-reusable;

(2) preserving (M3) the resolution of nucleic acid features on a first immobilized array during cycles of array replication involves amplifying the features of a first array to yield an array of features with a hemisphere radius (r) and a cross-sectional area (q) at the surface supporting the array, such that the features remain essential distinct;

(3) making (M4) multiple (N) comprising:

(a) providing a first liquid mixture of template nucleic acid, one oligonucleotide primer, which includes a linker moiety, and monomers capable of forming a polymerized gel matrix;

(b) contacting the mixture with a solid support;

(c) forming a first layer of a polymerized gel matrix with the linker moiety covalently bound to it;

(d) providing a second liquid mixture of one oligonucleotide primer and monomers capable of forming a polymerized gel matrix;

(e) contacting the first layer with the second liquid matrix;

(f) forming a second layer of a polymerized gel matrix;

(g) amplifying the template nucleic acid and transferring amplified nucleic acid to the second layer;

(h) removing the second layer; and

(i) optionally repeating steps (c) - (g);

(4) determining (M5) the nucleotide sequence of an immobilized nucleic acid array comprising:

(a) ligating a first double-stranded nucleic acid probe having a restriction endonuclease recognition site which is separate from the cleavage site, to one end of a nucleic acid of the array;

(b) identifying one or more nucleotides at the end of the polynucleotide by the identity of the first double stranded nucleic acid probe ligated to it or by extending a strand of the polynucleotide or probe;

(c) amplifying the features of the array using a primer complementary to the first double stranded nucleic acid probe, such that only molecules which have been successfully ligated with the first double stranded nucleic acid probe are amplified;

(d) contacting the amplified array with support such that a subset of nucleic acid molecules produced by the amplifying are transferred to the support;

(e) covalently attaching the subset of nucleic acid molecules transferred in the above step to the support to form a replica of the amplified array;

(f) cleaving the nucleic acid features of the array with a nuclease recognizing the nuclease recognition site of the probe such that the nucleic acid of the features is shortened by one or more nucleotides; and

(g) repeating steps (a) - (f) until the nucleotide sequences of the features of the array are determined;

(5) a method (M6) of determining the nucleotide sequence of the features of (N) comprising:

(a) adding a mixture comprising an oligonucleotide primer and a template-dependent polymerase to an array of immobilized nucleic acid features;

(b) adding a single, fluorescently labeled deoxynucleoside triphosphate to the mixture;

(c) detecting incorporated label by monitoring fluorescence;

(d) repeating steps (b) and (c) with each of the remaining three labeled deoxynucleoside triphosphates in turn; and

(e) repeating steps (b) - (d) until the nucleotide sequence is determined;

(6) a method (M7) of determining the nucleotide sequence of the features of micro-array of nucleic acid comprising:

(a) creating a micro-array of nucleic acid features in a linear arrangement within and along one side of a polyacrylamide gel, the gel further comprising one or more oligonucleotide primers and a template-dependent polymerizing activity;

(b) amplifying the micro-array of (a);

(c) adding a mixture of deoxynucleoside triphosphates, comprising:

(i) each of the four deoxynucleoside triphosphates; and

(ii) chain-terminating analogs of each of the deoxynucleoside triphosphates labeled with a spectrally distinguishable fluorescent moiety;

(d) incubating the mixture with the micro-array;

(e) electrophoretically separating the products of the extension within the polyacrylamide gel; and

(f) determining the nucleotide sequence of the features of the micro-array by detecting the fluorescence of the extended, terminated and separated reaction products within the gel; and

(7) a method (M8) for simultaneously amplifying multiple nucleic acids comprising:

(a) creating a micro-array of immobilized oligonucleotide primers;

(b) incubating the micro-array of step (a) with amplification template and a non-immobilized oligonucleotide primer;

(c) incubating the hybridized primers and template with a DNA polymerase and deoxynucleotide triphosphates; and

(d) repeating steps (b) and (c) for a defined number of cycles to yield multiple amplified DNA molecules.

USE - For nucleic acid replication or amplification, genomic

characterization, gene expression studies, medical diagnostics e.g. expression analysis and genetic polymorphism detection. They are also of use in DNA/protein binding assays and more general protein array binding assays. The methods are also useful for determining the sequences of nucleic acid on arrays.

ADVANTAGE - By using the novel nucleic acid arrays a full genome including unknown DNA sequences can be replicated. The size of the nucleic acid fragments or primers to be replicated can be from about 25-mer to about 9000-mer. The method is also quick and cost effective. The thickness of the chip is 3000 nm which provides a much higher sensitivity. The chips are compatible with inexpensive in situ polymerase chain reaction (PCR) devices, and can be reused as many as 100 times.

Dwg.0/10

L3 ANSWER 21 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

ACCESSION NUMBER: 2000-257012 [22] WPIDS

DOC. NO. CPI: C2000-078581

TITLE: Determining differential display of gene expression, useful for monitoring drug responses at the gene expression level and locating genes involved in a particular response, by comparisons between mono-length cRNA libraries.

DERWENT CLASS: B04 D16

INVENTOR(S): BELOUCHI, A M; FOURNIER, H; GAUVREAU, D; GEE, M

PATENT ASSIGNEE(S): (SIGN-N) SIGNALGENE INC

COUNTRY COUNT: 20

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000014273	A2	20000316	(200022)*	EN	73

RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE

W: CA JP

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000014273	A2	WO 1999-CA789	19990826

PRIORITY APPLN. INFO: US 1998-145936 19980903

AN 2000-257012 [22] WPIDS

AB WO 200014273 A UPAB: 20000508

NOVELTY - A (M1) of determining differential display of gene expression comprising comparisons of mono-length cRNA libraries, is new.

DETAILED DESCRIPTION - A (M1) of determining differential display of gene expression comprising comparisons of mono-length cRNA libraries, is new.

M1 comprises:

(a) preparing at least two substantially identical accessible ordered arrays (target arrays) of synthetic substantially mono-length oligonucleotide DNA segments representing permutations of possible oligonucleotide sequences;

(b) preparing partial length first cDNA library being a partial length segment library corresponding to substantially all complementary expressed mRNA sequences of a first gene source;

(c) using the library of step (b) and preparing a mono-length first cRNA library being a substantially mono-length segment library corresponding to or complementary with expressed mRNA sequences of the first gene source;

(d) preparing a substantially expression length first cDNA library

corresponding to or complementary with expressed mRNA sequences of the first gene source, where the library is a substantially expression length transcript library;

(e) preparing like-condition partial length second cDNA library being a substantially partial length segment library corresponding to or complementary with expressed mRNA sequences of a second gene source;

(f) using the library of step (e) and preparing like-condition mono-length second cRNA library being a substantially mono-length segment library corresponding to or complementary with expressed mRNA sequences of a second gene source;

(g) preparing like-condition substantially expression-length second cDNA library corresponding to or complementary with expressed mRNA sequences of the second gene source, where the library is a substantially expression -length transcript library;

(h) probe hybridizing the first and second mono-length segment libraries, each with an ordered array of step (a); and

(i) comparing the probe hybridized accessible ordered arrays to determine differential hybridization display sites between first and second mono-length segment libraries; and

(j) referencing differential hybridization sites to at least one of the expression-length libraries to locate the gene of expression differential.

INDEPENDENT CLAIMS are also included for the following:

(1) a mono-length segment cDNA library, where the mono-length segments comprise cDNA corresponding to substantially all complementary expressed mRNA sequences of a gene source;

(2) a vector insertable linker comprising a BssH II recognition site adjacent to an RNA polymerase promoter is in functional connection with a Bpm I recognition site readably adjacent to a Cla I recognition site which is adjacent to a Not I recognition site, which is adjacent to a Kpn1 recognition site which is adjacent to the RNA polymerase promoter site;

(3) a vector insertable linker comprising an RNA polymerase promoter site in functional connection with a Bpm I recognition site, adjacent to a Cla I/Msp I residual recognition site adjacent to an insert from a cDNA gene source adjacent to a Not I recognition site, which is adjacent to a Kpn1 recognition site which is adjacent to either the T3 or T7 RNA polymerase promoter site that is adjacent to the Bpm I recognition site;

(4) a mono-length cRNA library corresponding to complementary expressed mRNA sequence, where the library consists of cRNA elements 23 nucleotides in length and having the sequence of 5'-GCUGGAGAUCGGNNNNNNNNNNN-3' (N1), where the eleven n nucleotides correspond to a complementary 11 nucleotide sequences of the mRNA;

(5) a method (M2) of determining differential display of gene expression which is identical to M1 except steps (d), (g) and (k) of M1 are not carried out;

(6) a method (M3) of detecting a point mismatch probe nucleotide in short mono-length oligonucleotides derived from partial length segment or expression length segment oligonucleotide libraries comprising:

(a) hybridizing probe oligonucleotides against an accessible ordered array of synthetic short mono-length target oligonucleotide DNA segments representing all permutations of possible oligonucleotide sequences, where the probe oligonucleotides and the target site oligonucleotides are of substantially equal length; and

(b) quantitatively assessing hybridization sites;

(c) washing the hybridization sites under stringent conditions;

(d) detecting post-washing variation in hybridization sites representative of a point mismatch nucleotide; and

(e) referencing the site variation to a partial length or expression length segment of at least one of the libraries; and

(7) a mono-length gene tag library.

USE - The methods are useful for determining differential hybridization display sites between mono-length segment libraries and to

locate genes of expression differential.

The methods are useful in gene identification related to complex traits. The methods also permit monitoring drug responses at the gene expression level and locating genes involved in a particular response. The methods are also useful for pharmacogenomic research in evaluating how variability in genetic background influences positive or negative response to a drug.

ADVANTAGE - The methods overcome the problems associated with RNA quality, false positives and reproducibility encountered using prior art methods.

Dwg.0/4

L3 ANSWER 22 OF 23 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2000-206023 [18] WPIDS
CROSS REFERENCE: 2001-450361 [47]
DOC. NO. CPI: C2000-063736
TITLE: Analysis of polynucleotides using hybridization assays, useful for providing nucleotide sequences or relative concentrations which can be used in the prediction, diagnosis and treatment of diseases.
DERWENT CLASS: B04 D16
INVENTOR(S): HUNKAPILLER, M W; RICHARDS, J H
PATENT ASSIGNEE(S): (PEKE) PERKIN-ELMER CORP
COUNTRY COUNT: 22
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000009756	A1	20000224	(200018)*	EN	46
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE					
W: AU CA JP					
AU 9955601	A	20000306	(200030)		
US 6232067	B1	20010515	(200129)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000009756	A1	WO 1999-US18422	19990812
AU 9955601	A	AU 1999-55601	19990812
US 6232067	B1	US 1998-135381	19980817

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9955601	A	Based on	WO 2000009756

PRIORITY APPLN. INFO: US 1998-135381 19980817
AN 2000-206023 [18] WPIDS
CR 2001-450361 [47]
AB WO 200009756 A UPAB: 20010829

NOVELTY - Analyzing a polynucleotide (PN) comprises forming a representative restriction fragments (RF) corresponding to the PN, where the RF has two termini, at least one generated by a restriction endonuclease (RE), hybridizing, a terminus probe to a single strand of the RF at a position including the RE generated terminus, and an internal fragment probe adjacent to it, and joining the probes.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a PN population analysis kit comprising an oligonucleotide (ON) array comprising terminus probes, and internal probes;

(2) a PN population analysis kit comprising
(a) a sorting array comprising sorting signal receptors;
(b) terminus probes marked with the sorting signal, which is specific for the sorting signal receptors on the sorting array; and
(c) internal fragment probes labeled with a detectable label, where at least 2 of the internal fragment probes are labeled with different detectable labels; and
(3) a PN population analysis kit comprising
(a) a sorting array comprising sorting signal receptors;
(b) internal fragment probes marked with a sorting signal, which is specific for the sorting signal receptors on the sorting array; and
(c) terminus probes labeled with a detectable label, where at least 2 of the internal fragment probes are labeled with different detectable labels.

USE - The methods can be used for the simultaneous analysis of a large number of different PN molecules. They can be used to provide the nucleotide sequence, partial nucleotide sequence or relative concentrations of one or more different PNs in a complex PN composition. Analysis of large populations of PNs by the subject methods may be used to produce sufficient information about a PN population that differences between PN populations may be ascertained. The analysis methods can be used to predict, diagnose, or treat a variety of diseases.
Dwg.0/6

L3 ANSWER 23 OF 23 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

ACCESSION NUMBER: 1990:447565 BIOSIS
DOCUMENT NUMBER: PREV199090098205; BA90:98205
TITLE: SYNTHESIS AND CHARACTERIZATION OF NUCLEOSIDE PEPTIDES TOWARD CHEMICAL RNASES 1.
AUTHOR(S): BASHKIN J K [Reprint author]; GARD J K; MODAK A S
CORPORATE SOURCE: MONSANTO CO, ST LOUIS, MO 63167, USA
SOURCE: Journal of Organic Chemistry, (1990) Vol. 55, No. 17, pp. 5125-5132.
CODEN: JOCEAH. ISSN: 0022-3263.
DOCUMENT TYPE: Article
FILE SEGMENT: BA
LANGUAGE: ENGLISH
ENTRY DATE: Entered STN: 7 Oct 1990
Last Updated on STN: 7 Oct 1990

AB Site-selective cleavage of nucleic acids by chemical analogues of nuclease enzymes is an area of major interest. Since imidazole is known to catalyze the hydrolysis of RNA, we postulated that oligonucleotides with pendant imidazole groups could be used to hydrolyze RNA in a sequence specific manner, utilizing complementarity, the natural nucleic acid recognition mechanism. We report here the synthesis and complete characterization of a series of uridine-imidazole conjugates which are based on C-5 substituted deoxyuridine. The nucleoside is joined with a **variable-length linker** arm to histidine or related imidazole-containing moieties, and protecting groups were employed to allow the subsequent conversion of the nucleoside-peptides into phosphoramidites suitable for **oligonucleotide** synthesis. Extensive multidimensional NMR characterization of the novel nucleoside-peptides is reported.

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FULL ESTIMATED COST	124.23	124.86

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FULL ESTIMATED COST	2.22	127.08

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	0.00	-0.73

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